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GenCore version 5.1.6
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May 7, 2004, 12:59:49; Search time 9150.23 Seconds (without alignments) 10942.062 Million cell updates/sec 1 atgaaaaatgcacaactgaa.....caccacatattattgtctcg 2310 6940544 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: US-09-303-232-1_COPY_372_2681 2310 OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Scoring table: Sequence: Searched: Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a

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E58346 2886 bp DNA linear PAT 18-7HN-2001	insect actyl choline	E58346.1 GI:13019345 JP 2000023680-A/1.	Drosophila melanogaster (fruit fly) Drosophila melanogaster	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha;	purguantes, resepinitade; Drosophita. 1 (bases 1 to 288) Martin,A., Nadja,E. and Thomas,S. Nucleic acid encoding insect actyl choline receptor subunit
RESULT 1 E58346 LOCUS E	NO N	VERSION E KEYWORDS J	SOURCE D	MZA	REFERENCE 1 AUTHORS M TITLE N

ALIGNMENTS

CTGTTCAGAAGGATCGCAGCGAGCACCATCGCCTTCATTTCCTATTTAGGCAGCTTTGCA 780	901 TTATCTGCTAAAGTTTGCCTAGCAGGATATCATGAAAAAGAGCTGTTACACGATCTTTG 960	TITGGITTAACITTAATGCAAATTATCGATGTGGACGAGAAAATCAATTGCTAGTCACT 108	1081 AATGTGTGGTTAAAACTGGAGTGGAACGACATGAATCTCGGCTGGAACACCTCCGACTAT 1140	TACAACAGTGCGGATGAGGGATTTGACGGCACCTACCAGACGAACGTGGTGGTGCGGAAC 12	1261 AACGGCTCGTGTCTATACGTTCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATC 1320	1692 ACGTGGTTCCCCTTCGATGACCAGCGGTGCGAGTGAAGTTCGGCAGTTGGACCTACGCC 1751 1381 GGATTCCAGCGATTTACAATTACAAGATGAACTGGCGGTGATATCAGAGTTGCAGGG 1440 1752 GGATTCCAGCTGATTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTG 1410 1752 GGATTCCAGCTGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTG 1811	812	193	TACTATTTCT	2 TTCACCCTGCCGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCG 205 1 CTGACCGTGTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCTC 1 CTGACCGTGTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCA 174	2052 CTGACCGTGTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCA 2111 1741 TTGTGGATACGCATCGTGTTTTTGTGCTGCCATGGATATTGCGAATGAGTCGCCA 1800 2112 TTGTGGATACGCATCGTGTTTTTGTGCTGCCATGGATATTGCGAATGAGTCGCCCA 2171 1801 GGACGACCGCTGATCCTAGAGTTCCCGACCACGCCCTGTTCGGACACATCCTCCGAGCGG 1860
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JOURNAL Patent: JP 2000023680-A 1 25-JAN-2000; BAYER AG COMMENT OS ED-2000023680-A/1 PN JP 2000023680-A/1 PD 25-JAN-2000 PP 26-APR-1999 JP 1999118159 PR 04-MAY-1999 DB 19819829.9 PT MARTIN ADAMUTSUEUSUKI,NADJA ERASU,THOMAS SCHULTE PC C121N15/09,A01K67/033,C07K14/705,C07K16/28,C12N1/21,C12N5/10, PC C12Q1/68, PC G01N33/15,G01N33/50//(C12N1/21,C12R1:19),C12N15/00,C12N5/00 CC	FH Key Location/Qualifiers FT CDS (372). (2681). FEATURES Location/Qualifiers source 1.2886 / Organism="Drosophila melanogaster" / mol_type="genomic_DNA"	/db_xrel="taxon:/22/" ORIGIN Query Match	ATGADADA ATCACCA ATGACTGA CTGACTTGA CGATGATGATGATGATGATGATGATGATGATGATGATGATG	Db 432 AGATTAGCGCACTGCAGCAGCACTTTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	181 CACAGCAACATTGCAAGCGAGCACAATAGCCAGCAACAACAGCAGCAGCATCGAAGGAC 24	Qy 241 GAGGATGAGCGACCACGGATGAGGAATGACCAGCAACGGATCTGCAACAGCTAGAC 300 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 672 AGCAGCAACATGTTGTCGCCAAAGACAGCCGCAGCAACTGCTGCCGGCGATGAAGCA 731 Qy 361 ACAACCCAACAACAACATAAGACTGTGTGCACGCAAGCGACAACGATTGCGTCGC 420 Db 732 ACAACCCAACAACAACATAAGACTGTGTGCCACGCAAGCGACAACGATTGCGTCGC 791	421 CGACGAAAAAGAAAACCAGCAAACGAAAACAGAAATATCAAGAAAACAACTT 48 	481 AGCATGCCTTCAAAACGCGCAAATCCACGGACACTACAGCACCACCAGCAACA 5 	Qy 541 ACCAGCTGTCCGACAGCCACCTACATGTCGAGCCAGGGACAATGAGTTCAGTATT 600 Db	972 CCGAIAICGAGACAIGAIAGAGIAICCACGGCCACAITCGCCTGGGTGITGCTG 1 661 CAGGIGCTGCTCGTGCTGCAACAGTGGCACTTCACGTGCAACAGCCATGGCTG 7 1032 CAGGIGCTGCTGCTGCTGCAACAGTGGCAACTTCACGTGCAACAGCCATGCGTGCTA 7 1032 CAGGIGCTGCTGCTGCTGCAACAGTGGCAACTTCACGTGCAACAGCGAICGGTGCTA 1

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VLOVILIVSLOQMQLHYQRSVILFRIAASTTAFISYLGSPAAQLESSSSSSNSSNSSN
GNSSSTQILNGINKHSWIPLLIYINLSAKVCLAGYHEKRLHDLLDPYNTLERPVLNE
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RIWKPDVLAYNSASDEGFDGTYQTNVVVNNVKLEWNDNNLRWYTSDYGGVKDLRIPPH
CEMKFBOYLAYNSASDEGFDGTYQTNVVVNNVSCLYVPPGIFKSTCKIDITWFFFDDQR
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Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B. Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalphas, Dalphas, and Dalpha; In Drosophila melanogaster Identify; New and Highly Conserved Target of Adenosine Deaminase Acting on Genetics 160 (4), 1519-1533 (2002)
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Drosophila melanogaster nicotinic acetylcholine receptor Dalphas subunit (nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds, alternatively spliced.
AY036613 GI:20340268
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/note="ion channel; neurotransmitter transmembrane
receptor; exon 5 is excluded due to exon skipping,
generates a loss of reading frame and a truncated
polypeptide; alternatively spliced"
/codon_start=1
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1 3QX, UK
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Grauso,M. and Sattelle,D.B.
Direct Submission
Submitted (26-MAY-2001) MRC-FGU Human Anatomy and Genetic University of Oxford, South Parks Road, Oxford OX1 3QX, Location/Qualifiers
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Drosophila melanogaster
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/db_xref="G1:20340269"
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/db_tref="texter"

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/chromosome="2"

/map="34E4-34E5"
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                          CTCAACGGCGAGTGGGAACTACTGGGGTGTGCCCGGCAAACGTAACGAGATCTATTACAAC
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                                                                                                   TGCTGCCCGGAACCCTATATAGACATCACCTTCGCCATCATCATCCGCCGACGAACACTG
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3 (Calniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Centerr, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
                                                                                                                                                                                                                                                                                                             14290 IGGICTICTIACAATIGCAGAAACAACAACTIAGCATGCCTCCCTTCAAAACGCCC
                                                                                                                                                                                                                                                                      AATCCACGGACACCTACAGCACACCAGCAACAACCAGCTGTCCGACCAGCCACCTACA
                                                                                                                                                                                                                                                                                                                                                                                                   TGCAATGTCGAGCCAGCGACAATGAGTTCAGTATTCCGATATCGAGACATGATAGAGTAT
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           915
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rerriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kurse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Padleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phouanenavong,S., Pittman,G.S., Puri,V., Richlards,S., Scheeler,F.,
Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berkeley, CA 94720.
This sequence was assembled using end sequences from a whole genome shotgum and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14711
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                                                                                                                                                                                                                                                                                                       Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GAGGATGTAGCCAACCACGGTAGAAGCAATGACCAGCAGGAGCCATGTGCAACAGGTAGAC 300
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/clone_lib="RFCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 158758;
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Pred. No. 3.4e-201;
0; Mismatches 13;
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/strain="Y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2L"
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1. .158758
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Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Pácleb, S., Pfeiffer, B., Pfolalfer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Direct Submission

L. Direct Submission

Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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                                                                                                                                                                                                                                                                                                                                    Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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/clone ||Ib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.6%; Score 776.2; DB 3; Length 186803; 89.0%; Pred. No. 3.6e-201; ive 0; Mismatches 13; Indels 98;
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1. .186803
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Ballew, R. M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E. M., Ballew, R. M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E. M., Beeson, K. Y., Benos, P. V., Berman, B. P., Bhandari, D., Bolshakov, S., Borkova, D., Borthan, R. R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Busam, D. A., Butler, H., Cadieu, E., Center, A., Chandra, I., Cherry, J. M., Cawley, S., Dahlke, C., Davenport, L. B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A. D., Dew, I., Dietz, S. M., Dodson, K., Doup, L. E., Downes, M., Dugan-Rocha, S., Perrierz, C., Dunn, P., Durbin, K. J., Evangelista, C. C., Ferraz, C., Ferriera, S., Pleischmann, W., Fosler, C., Gabrielian, A. E., Garg, N. S.,

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                                                                                                                                                                                                                              codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (O-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases I to 272521)
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Submitted (23-JAN-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
On Sep 16, 2002 this sequence version replaced gi:7298121.
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Marara, C. Crosby, M.A., Matthews, B.B., Bayraktaroglu, L.,
Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochnik, S.E.,
Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W.,
Celniker, S.E., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., de
Grey, A.D. N.J., Harris, N.L., Kronniller, B., Marshall, B.,
Milburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E.,
Shu, S., Smutniak, F., Whitfield, E.J., Ashburner, M., Gelbart, W.M.,
Rubin, G.M., Mungall, C.J. and Lewis, S.E.
Annotation of Drosophila melanogaster genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (bases 1 to 272521)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA (bases 1 to 272521)
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Elydycidea; Drosophiladae; Drosophila.

Ashburner, M., Misra, S., Roote, J., Lewis, S.E., Blazej, R., Davis, T., S. Doyle, C., Galle, R., George, R., Harris, N., Harris, N., Harris, N., Harris, N., Harris, C., Moshrefi, A., Palazzol, M., Reses, M.G., Spradling, A., Tsang, G., Man, K., Whitelaw, K., Celniker, S. and Rubin, G.M.

An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region

Cenetics 153 (1), 179-219 (1999)
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104365 ATAAACACTCATGGATATTTTATTGATATTTTGAATTTATCTGCTAAAGGT 104417
                                                                    GCAGCAGCAGCAGCAACAACAGCAACAACAACAGCAGCACGCAAATATTAAACGGACTTA
                             AGTGGCAACTTCACGTGCAACAGCGATCGGTGCTACTGTTCAGAAGGATCGCAGCGAGCA
                                                                                                                                                     Submitted (08-MAR-2000) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, MS 64-121, Berkeley,
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                                                                                                                                                                                                                                                                                                                                                                        /db_xref="FLYBAGE:FBGN0028542"
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ASGFENDRKSAECLEVGLNGVCVGNNQCDCKTGYVRDEHQRNICQPHCPQGCQN
GYCSAPNFCICRPGFIKSGIKGRQTCQAV"
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/note="8ynonym: CG16882; last curated on Mon Nov
13:14:17 PST 2002"
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/gene="BG:DS00180.8"
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On or before Mar 22, 2000 this sequence version replaced gi:2337897, gi:2337897, gi:2337897, gi:2337897, gi:3097819, gi:305578, gi:3097819, gi:3097819
                                                                                                                                                                                                                                                                                                                                                                                    The orientation of this sequence along the chromosome is left to right. This sequence was annotated by Sima Misra (sima@fruitfly.berkeley.edu) on behalf of the Berkeley Drosophila Genome Center. Coding sequences are predicted based on computational analysis, using both gene and CDS prediction programs and matches to other sequences. These predictions and matches been evaluated by the annotators and may have been refined by hand. The annotators have also used their judgement about which matches to include in this record. The annotations on this sequence can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.fruitfly.org/publications/Adh.html
The annotation syntax used in this record is documented at
ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.v
1.2.
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[05-Feb-1998] [Build sol2.5-ultra 01:47:35 05-Feb-1998]'',
score:'329.0'', desc:'GenBark:189383:H.sapiens mRNA for
RNA specific clitase. CDS:148. .225; PID:e254628;
PID:91707504.'', species:'Homo sapiens"
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SSLNFCCDDAQLESLERAIFKRFDCRTFKHTRFQPQRPQINIDPGIRFBFSQRSDWQP
SPNGLIWSQVPEELRPYEISVNGKRQGVTKKKMKTSQAALAISKYKLFLTFLELVKFN
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mol type="genomic DNA"
strain="y; cn bw sp"
db_xref="taxon:727"
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/product="hypothetical_protein"
/protein_id="AAF44818.1"
/db_xref="GI:7287780"
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1572. . 1681,1752 . 1912,1978 . 2283,2405 . 2560)

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1501. 1617. . 1681,1752 . 1912,1978 . 2283,2405 . 2560)

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                     Length 320754;
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                      33.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 [bases 1 to 1683]
Millar, N.S.
Direct Submission
Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WC1E 6BT, UNITED KINGDOM
DMES54210 1683 bp mRNA linear INV 01-APR-200 Drosophila melanogaster mRNA for nicotinic acetylcholine receptor subunit Dalpha7 (nAcRalpha-18C gene).
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                                                                                                                                                                                                                    subunit
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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nAcRalpha-18C gene, nicotinic acetylcholine receptor
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Pred. No. 7e-130;
0; Mismatches 436;
                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
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/organism="Drosophila
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1. .1683
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132. .1651
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/gene="nAcRalpha-18C"
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Best Local Similarity 62.5%;
Matches 952; Conservative
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TCAACTGAATATGAATTAGGTTPA TCTGCGGAGTACGAACTGCGCTC CGTAAAGATGACGAACTGCAATGAC GTAAAAGAGGACGAAACAGAGGGA AAAAAGAGGACGAAACAAAC	SULT 11 143846 CUS FINITION CESSION RSION RSION RRICH TREE TREE TREE TREE TREE TREE TREE TRE	CE RS	JOURNAL Submission JOURNAL Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. Q 18,, Leverkusen 51368, Germany FEATURES Location/Qualifiers 1. 3529 Ag 29	0 (4)78823804	Query Match 22.2%; Score 512.8; DB 3; Length 3629; Best Local Similarity 62.5%; Pred. No. 4.3e-129; Indels 24; Gaps 4; Qy 925 GGATATCATGAAAAGACTGTTACACGATCTTTTGGATCCTTATAATACACTAGAACG 984 Db 425 GGGTACCACGAGAAGCGGCTACTGCACCACCTATTGGACCACTACTACGACGG 484
QY 1153 GATCTGCGATACCGCCGATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCG 1212 Db 359 GATCTGCGAATTCGCCCACATCGCCTATGGAAACCGGATGTACTACAACAGTGCC 418 QY 1213 GATGAGGGATTTGACGCACCTACCAGACGTGGTGCTGGTGCTGGTGTTCTTTTTTTT			CCTC 1 CCTC 1 GTTT 1 ATTC 1 ATGR 1 ATGR 1	TTCCGGACGCCGGGACGACGACCCTCCGAGGGAAGCACCAGATACTCTCC	1999 GCTTTCTATCGCACGGTTTATGGACAAGGCGACGATGGCAGCATTGGCCAGT 2058 1313 ACATATTACAGGACGATGACAGGCAGGACGATGGCAGCACCATTGGCAGC 2058 1313 ACATATTACAGGACGATGACAGGAGGATGACGCAGGACCGTGGGACCA 1372 2059 AC

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Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: EP 0962528-A 3 08-DEC-1999;
BAYER AG (DE)
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                                                                                                              GTCGACTACGAGCTCTCCCTCATTCTGAAGGAGAATTAGAGTCATCACAGATCAGATGCGC
                                                                      ACTGAATATGAATTAGGTTTTAATCTTAAAGGAAATTCGCTTTATAACTGATCAGCTACGT
                                                                                                                                                                               AAAGATGACGAGTGCAATGACATTGCCAATGATTGGAAATTTGCAGCTATGGTCGTTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera, Endopterygota, Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae, Heliothinae; Heliothis.
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                TACAGGGGGGGGAGAATGGCGCGGGGTTGGCGGCGCGCACAGTTGCTTC
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/db_xref="taxon:7102"
335 .1825
/note="unnamed protein product"
/codon_start=1
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Pred. No. 4.3e-129;
0; Mismatches 502;
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Sequence 3 from Patent 1
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Best Local Similarity 62.5%;
Matches 878; Conservative
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VERSION
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AX009612
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Culetto, E. and Sattelle, D.B.
Rorauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
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ERPVANESEPLEVKFGLTLQQIIDVDEKNQILTTNAMINLEMNDYNIKWNETEYGGW
ELTIPRKLKKRDVLLAYNBAGGFDGTYHTNIVVKHGSCLYVPPGIFKSTCKIDITW
FPFDDQHCBKKFGGYTTDGNQLDJLNSEDGGDLSDFTTNGFWYLLANGKTGYTDTY
CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDGGEKTTGYTIT
ELSTTVELNIVARETLEQVSDAIPLGFTFNCIRGHWASSVLLTVVLVNYHHRTADIHEM
FPRITSGSQTAIGSSASFGRPTTVEEHHTALGCHKDLLLIKELGFTARDD
FFRHTSGSQTAIGSSASFGRPTTVEEHHTALGCHKDLLLIKELGFTTARMKEDD
2023 bp mRNA linear INV 29-APR-2002 nicotinic acetylcholine receptor Dalpha6 (nAcRalpha-30D) mRNA, complete cds,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OXI
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Bukoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/chromosome="2"
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/note="results in isoleucine
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/protein id="AAM13392.1"
/db_xref="G1:20152845"
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/gene="nAcRalpha-30D"
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GTTTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTGTGGAT 1748
          TTTCAATTTAATCGTGCCATGTGTGCTAATCTCATCGATGGCCCTACTGGGCTTCACATT 1160
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Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify New and Highly Conserved Target of Adenosine Deaminase Acting on Genetics 160 (4), 1519-1533 (2002)
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                                                                                                                                                                                                                                                              1749 ACGCAICGIGITITIGIGCIGCCIGCCAIGGAIAITIGCGAAIGAGICGCCCAGGACGACC
                                                                                                                                                                                                                                                                                                                1281 CACCTACTICAATIGCATCATGTTCATGGTCGCCTCGTCGGTGGTGCTGACAGTAGTGGT
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein id="AAM13394.1"
db xref="G1:20152849"
'translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FPFDDQHCEMKFGSWTYDGNQLDLVLNSEDGGDLSDFITNGEWYLLAMPGKKNTIVYA
CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSLTVFLNLVAETLEQVSDAIPLLGTYFNCIMPMVASSVVLTVVVLNYHRTADIHEM
PPWIKSVFLGWLPWILRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDD
DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to serine substitution; compared in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                      8p
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DLRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHSGSCLYVPPGIFKSTCKNDITW
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/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
                                                                                                     OXI
                                                                                                                                                                                                                                                                                                                                                                                 'note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681 CAAGGATCTACGAATCACGCCCAACAAGCTGTGGAAGCCCGACGTGCTCATGTACAACAG
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                    2 (bases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford (
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Pred. No. 1.4e-109;
0; Mismatches 574;
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to the sequence deposited
AE003626"
                                                                                                                                                                                                                                                                                                                                            179. .1863
/gene="nAcRalpha-30D"
                                                                                                                                                                                                    mol_type="mRNA"
db_xref="taxon:7227"
chromosome="2"
                                                                                                                                                                                                                                                                                                                       'gene="nAcRalpha-30D"
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                                                                                                                                              Location/Qualifiers
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1821 GGTTACGGTGCTGCGCTCCGCACATAATCGT 1856 Dp

Search completed: May 8, 2004, 02:41:13 Job time : 9171.23 secs

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- nucleic search, using sw model OM nucleic

7, 2004, 10:08:00 ; Search time 929.055 Seconds (without alignments) 10562.710 Million cell updates/sec Мау Run on:

US-09-303-232-1 COPY 372 2681

1 atgaaaaatgcacaactgaa.........caccacatattattgtctcg 2310 Perfect score: Sequence:

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues Searched:

6747726

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqn2001as:*
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geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* N_Geneseq_29Jan04: geneseqn1980s:* geneseqn1990s:* geneseqn2004s:* geneseqn2000s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abl27131 Drosophil Abl27130 Drosophil Abl07799 Drosophil Aaz24476 H. viresc Drosophil Drosophil H. viresc Drosophil Human PRO Human neu Neuronal Human neu Human neu Mutant hu Mutant hu V274T var Mutant hu Human pol Neuronal melano Wild-type Human neu Neuronal Description Abl13733 I Abl07231 D Abl07798 I Abl07798 Aac58395 R Aac90380 W Aav12197 H Aav12197 H Abs54875 R Abs54875 R Abs54876 H Abs73248 H Abs73248 H Aac90385 N Aac90386 N Aav44687 N Aac90387 N Aat59197 N Abz11298 H SUMMARIES ABL27130 ABL07799 AAZ24476 ABL13733 ABL07231 AAZ24477 ABL07798 AAC58395 AAC90380 AAV12197 AAT48239 ABS54875 ABV73248 ADA10864 AAC90385 AAC90386 AAT59197 ABZ11298 AAT59196 AAV44687 AAC90387 AAZ24475 DB Length 936 1540 3109 14668 1509 1876 1876 1876 1876 1509 1509 1509 1509 2101 1964 2769 2886 984 3700 1876 Query Match 1 17.8 17.8 112.8 112.8 112.8 112.8 112.8 112.8 112.8 112.8 112.3 2310 881 766.2 5310 612.3 4411.2 4411.2 296.2 296.2 296.2 296.2 296.2 296.2 296.2 296.2 296.2 294.6 294.6 283.8 267.8 Score 284.4 Result

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ALIGNMENTS

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds. D. melanogaster acetyl-choline receptor DNA from clone Da7. /*tag= a /product= "acetyl choline receptor." AAZ24475 standard; cDNA to mRNA; 2886 BP Location/Qualifiers 372. .2684 (first entry) Drosophila melanogaster. 17-FEB-2000 AAZ24475; RESULT 1 Key AAZ24475

98DE-01019829 DE19819829-A1. 04-MAY-1998; 11-NOV-11999

98DE-01019829 (FARB) BAYER 04-MAY-1998;

Schulte T; Adamczewski M, Oellers N,

WPI; 2000-014207/02. P-PSDB; AAY50814 New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Claim 1a; Page 8-12; 26pp; German.

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as

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AAGCACCAGATACTCTCCGACGTTGAGCTGAAAGAGCGCTCGTCGTCGAAATCGCTGGCC
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                                GATCCTTATAATACACTAGAACGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGC
                                                TTTGGTTTAACTTTAATGCAAATTATCGATGTGGACGAGAAAAATCAATTGCTAGTCACT
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    insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster
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                                                                       Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 U; 0 Other;
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ive 0; Mismatches
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1es 2310; Conservative
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                                                                                                                                                                            TCATCAACTGAATATGAATTAGGTTTAATCTTAAAGGAAATTCGCTTTATAACTGATCAG
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                              CACAGCAACATTGCAAGCGAGCACACTAGCCAGCAACAGGAGCCAGGATCGAAGGAC
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                                                                                                      developmental biology; cell signalling; insecticide;
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                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 32863
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                           isolated nucleic acid detection reagent for detecting 1000 or more as from Drosophila and for elucidating cell signaling and cell-cell
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88.4%; Pred. No. 1.8e-138;
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurotransmission; plant protection agent; conductance; AChR; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nicotinic; insect; insecticide;
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AAZ24476 standard; cDNA to mRNA; 3700 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7137-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
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Best Local Similarity 73.5%; Pred. No. 8.3e-124;
Matches 611; Conservative 0; Mismatches 220;
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Drosophila melanogaster expressed polynucleotide SEQ ID NO 16175
                                                                             developmental biology; cell signalling; insecticide;
                 ВР
                 CDNA; 1540
                                                                                                                                                                2000US-0191637P,
2000US-00614150.
                                                                                                                                                23-MAR-2001; 2001WO-US009231
                                              (first entry)
                                                                                                   Drosophila melanogaster
                                                                                    gene;
                 standard;
                                                                                                                                                                                       (PEKE ) PE CORP NY
                                                                                    pharmaceutical;
                                                                                                                  WO200171042-A2
                                                                                                                                                                        11-JUL-2000;
                                              26-MAR-2002
                ABL07231
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1540 BP; 412 A; 390 C; 376 G; 362 T; 0 U; 0 Other;
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TGAAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGT 1703
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                                   CATTGACGTGGACGAGAAGAATCAACTTATAACCAATATATGCTGTCGTTGGAGTG
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          1044 TATCGATGTGGACGAGAAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAACTGGAGTG
                                                                          GAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAAT
                                                                                                          GNATGACTACAACCTGAGGTGGAACGACGAGGTATGGCGGGGTCAAGGACCTCAGGAT
                                                                                                                                            1164 ACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTGCGGATGAGGGATT
                                                                                                                                                                            391 caceccaacaagrieredaaaecedaacerrarerararaaaagreereaacaaearri
                                                                                                                                                                                                                  TGACGCACCTACCAGACGACGTGGTGCTGCGGAACAACGGCTCGTGTCTATACGTTCC
                                                                                                                                                                                                                                                451 TGACGGGACCTACCAGACCAACGTGGTCAGAAGCGGCGCGCAGTTGCCTGTACGTGCC
                                                                                                                                                                                                                                                                                  1284 GCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCCCCTTCGATGACCA
                                                                                                                                                                                                                                                                                                              511 ACCTGGCATATTCAAGAGCACATGCAAGATGGACATGGCGTGGTTTCCCTTCGACGACCA
                                                                                                                                                                                                                                                                                                                                                  1344 GCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGCTGGATTTACAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1464 GGGTGTGCCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCCGGAACCCTATATAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCCGAGACCCTGCCACAGGTCTCCGACGCTATCCCCCTGT
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11-JUL-2000; 2000US-00614150.
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ABL07798
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                                                                                                   885
                                 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) gense which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 AccedigeccaAceaeaceaAcceciaeaecteaestcaesiicaeciigacciigacaeaeaa
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                                                                                                                                     CCGIGITICIGAATAIGGIIGCCGAGACAAIGCCGGCIACTICCGAIGCGGIGCC 1739
                                                                                                                                                          screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                           Acetyl-choline receptor; nicotinic; insect; insecticide; screenir
neurotransmission; plant protection agent; conductance; AChR; ds
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                                                                                                                                                                                                                                                                                                                                                           H. virescens acetyl-choline receptor DNA from clone Hva7-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 411.4; DB 3; Length
Pred. No. 1.7e-104;
0; Mismatches 256; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor isolated from Heliothus virescens
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Best Local Similarity
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     1565
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inflammatory disorder; immunologic disorder;
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                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                           solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1053 GGACGAGAAAATCAATTGCTAGTCACTAATGTGTGTGTAAAACTGGAGGGGAACGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                   Sequence 14668 BP; 4616 A; 3078 C; 2662 G; 4312 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                  .8; DB 4; Length 14668; 7.4e-83;
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                                                                                                                                                                    Claim 1; SEQ ID NO 17876; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Score 335.8;
Pred. No. 7.4
                                       Myers EW;
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                                   PWD,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 337; Conservative
                                                                                                           New isolated nucleic
                                     Adams M,
                                                                2001-656860/75
       CORP NY.
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                                                              WPI; 2001-656860
P-PSDB; ABB63695
                                                                                                                                           interactions.
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                                   Venter JC,
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      (PEKE )
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO390, PRO341, PRO355, PRO619, PRO1030, PRO1030, PRO1030, PRO1030, PRO1030, PRO1030, PRO1030, PRO1030, PRO1030, PRO1031, PRO1101, PRO1103, PRO1030, PRO1031, PRO1101, PRO1101, PRO1103, PRO1184, PRO1187, PRO1181, PRO2198, PRO2198, PRO3197, PRO1101, PRO2194, PRO2194, PRO2195 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO2198 PRO antagonists can be used to inhibit tumour cell growth. The PRO2198 PRO antagonists can be used to treat various conditions, including those characterised by Overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, confident and juganoies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, arrowal and blastocoelic disorders, and inflammatory, angiogenic and hypothalsation probes used in the isolation of the human PRO sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 ACGIGICCCIGCAAGGCGAGIICCAGAGGAAGCIIIACAAGGAGCIGGICAAGAACIACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO polynucleotides encoding PRO polypeptides, useful in sut, diagnosis and prevention of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 296.2; DB 3;
Pred. No. 2.9e-72;
0; Mismatches 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 50; Fig 57; 286pp; English.
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99US-0141037P.
99US-0143048P.
99US-0145698P.
99WO-US0208313.
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60.7%;
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Best Local Similarity 60.7°
Matches 506; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-572270/53.
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                                                         WO200053755-A2
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                                                                                                                                                                              06-JAN-2000;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe CK,
                                                                                                                                                                                                                                                                                                                                   07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1999;
                                                                                                                                                                                                                                          08-MAR-1999;
                                                                                                                                                                                                                                                                          02-JUN-1999;
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                                                                                                                  14-SEP-2000
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                                            Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
                                                                                                                                                                                                                                                                                                                                                                              970
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                                                                                                                                           The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AxC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCTATACGTTCCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCC
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                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                             0; Mismatches 318;
                                                                                                                                                                                                                                                                                                              Score 296.2; DB 4
Pred. No. 2.9e-72;
                                                                                                                 Example 5; Page 60-61; 77pp; English
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Best Local Similarity 60.7%;
Matches 506; Conservative
WPI; 2001-061524/07.
P-PSDB; AAB50012.
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                                                                                                                                                                                                                                                    GCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCGATGTACGCTGGTTTC
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                                                recaaargrerregacagarcacrarrracagregaargrercagaararecagggrea
                                                                                    AGGATCTGCGAATACCGCCGCATCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTG
                                                                                                                    AGACTGTTCGTTTCCCAGATGGCCAGATTTGGAAACCAGACATTCTTCTCTATAACAGTG
                                                                                                                                                       CGGATGAGGGATTTGACGGCACCTACCAGACGAGGTGGTGGTGCGGAACAACGGCTCGT
                                                                                                                                                                             GTCTATACGTTCCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TICTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wild-type human alpha7 ligand gated ion channel coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, alpha7 nicotinic acetylcholine gated ion channel, 5-hydroxytryptamine, 5-HT3; calcium ion conductance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkenpas MB;
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                                  ATCCTTGGAGAGGCCGTGGCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGA
                                                                      1031 CTTTAATGCAAATTATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGG
                                                                                                    GCCTCCTGCAGATCATGGACGTGGAGGAACCAAGTTTTAACCACCAACATTTGGC
                                                                                                                                                                                                      AGGATCTGCGAATACCGCCGCATCTGGAAGCCGGACGTGCTGATGTACAACAGTG
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        ATACACTAGAACGTCCCGTTCTCAATGAATCGGACCCGGTTACAATTAAGCTTTGGTTTAA
                                                                                                                                     TAAAACTGGAGTGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTA
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                                                                                                                                                                                                                                                                                                       CTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits on specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with none or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 ACGTGTCCCTGCAAGGCGAGTTCCAGAGGAAGCTTTACAAGGAGCTGGTCAAGAACTACA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human neuronal nicotinic acetylcholine receptor subunits and DNA - also transformed cells useful for screening cpds. which modulate activity of
911 AAGTTTGCCTAGCAGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCTTATA
                                                                                                                                                                                                                                             Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA
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/product= "neuronal nicotinic acetylcholine receptor
alpha-7 subunit"
                              TTCTGAATATGGTTGCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743
                                                                                                                                                                                                                                                                                 il nicotinic acetylcholine receptor; alpha-7 subunit;
screening; NAChR; antibody; ds.
                                                      TCATGCTGCTCGTGGCTGAGATCATGCCCGCAACATCCGATTCGGTACCATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 0 U; 1 Other;
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Best Local Similarity
Matches 506; Conserv
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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human nNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human nNAChR polypeptide
AGCCCTACCCGATGTCACCTTCACAGTGACCATGCGCCGCAGGACGCTCTACTATGGCC
                                                          TCAACCTGATCATACCTTGTGTACTGATTGCCTCCATGGCCTTGCTCGGATTCACCCTGC
                                                                                        TCAACCTGCTGATCCCCTGTGTGTCTCTCCGCCCTCGCCCTGCTGGTTCCTGCTTC
                                                                                                                                    CGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCGCTGACCGTGT
                                                                                                                                                                         crecaearrcceeseagaarrrcccresesaraacaercrracrcrcrraccerr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human neuronal nicotinic acetylcholine receptor alpha 7 subunit cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nicotinic acetylcholine receptor; nNAChR; gene; ss; 7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to
                                                                                                                                                                                                                                                   rcargerecrescreagarcarsecescaacarecgarrescrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nNAChR alpha 7 subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 101; Col 57-60; 56pp; English
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73. .1581
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08-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                            of the
                                                                                                                                                                                                                                                                                                                                                                                                  esb.
                                                                                                                                                                                                                                                                                                                                                                        A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) of th human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp mammalian cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for identifying cpds. that modulate the activity of human nAChRs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCG
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                                                                                                                                                                                                                                                                             Nucleic acids encoding nicotinic acetyl:choline receptor sub-units in screening to determine the effect of drugs on the receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 296.2; DB 2;
Pred. No. 3.3e-72;
); Mismatches 318;
                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 71-73; 108pp; English
                                                                                                                                          (SIBI-) SIBIA NEUROSCIENCES INC
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                                                                  96WO-US009775.
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nes 506; Conservative
                                                                                                                                                                               Harpold MM,
                                                                                                                                                                                                                       WPI; 1997-065463/06.
P-PSDB; AAW09025.
                                                                  07-JUN-1996;
                                                                                                      07-JUN-1995;
                                                                                                                                                                                 Elliott KJ,
                            27-DEC-1996
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immunochemistry; NAChR alpha7 subunit;

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Ношо Key

Location/Qualifiers

73. .1581 /*tag= a /product= '

/product= "NAChR alpha7 subunit" /note= "neuronal nicotinic acetylcholine receptor"

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          Length 1876;
                                                                             Indels
                                                                         0; Mismatches 318;
          DB 6;
       Score 296.2; DB Pred. No. 3.3e-72
       12.8%;
60.7%;
                                                                      Conservative
                                   Similarity
                                                               206;
Query Match
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beta subunits of in vitro screening

Cell comprising nucleic acids encoding human alpha and be neuronal nicotinic acetylcholine receptors, useful for in of a drug substance in a test system specific for humans.

Elliott

ъ,

Siegel

Chavez-Noriega LE,

Claeps

Gillespie A,

2002-698532/75.

P-PSDB; ABB82435

29-OCT-2001; 2001WO-US050985 01-NOV-2000; 2000US-00703951

WO200259266-A2

01-AUG-2002

(MERI) MERCK & CO INC

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The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NAChR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NAChR alpha7 subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .031 CTTTAATGCAAATTATGGATGTGGACGAGAAAAATCAATTGGTAGTCACTAATGTGTGGT
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60.7%; Pred. No. 3.3e
cive 0; Mismatches
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424

Human; neuronal; nicotinic acetylcholine receptor; NAChR; drug screening;

Human neuronal NAChR alpha7 subunit encoding cDNA

22-JAN-2003

standard; cDNA; 1876 BP

ABV73248 ABV73248

RESULT 15 ABV73248

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1391 TGGATTTACAATTACAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCG 1450
                                                                                                                                                                                                                                    1451 AGTGGGAACTACTGGGTGTGCCCGGCAAACGTAACGAGATCTATACAACTGCTGCCGG 1510
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                                                                                                                                                                                                                                                                                                                                                                      1631 CGCCAGATTCGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGT 1690
                                   1271 GICIAIRACGIICCGCCGGGGAICTICAAGICGACGIGCAAGAICGACAICACGIGGIICC 1330
                                                                                                1331 CCTTCGATGACCAGCGGTGCGAGATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGC 1390
                                                               485 GCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCGATGTACGCTGGTTTC 544
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Search completed: May 7, 2004, 15:01:30 Job time: 939.055 secs

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7, 2004, 14:08:32 ; Search time 6207.93 Seconds (without alignments) 1111.850 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

em_estba:*
em_esthum:*
em_estin:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. gb_gss1:* gb_gss2:*

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	Description	BG632919 GH16126.3 AL058211 Drosophil AL073676 Drosophil AL064281 Drosophil
SUMMARIES	ID	BG632919 CNS0001F CNS00HJU CNS006F9
	DB	12 29 29 29
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₩		118.4 124.3 124.0
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2000	CD013901 90134548 BU915857 AGENCOURT	~	Mus m	~	373	m.	N I	22.5	AKUZYI// MUS MUSCU	160 K-RST020	2875	3497 Mus	730 Mus	Mus	Mus	Mus	Mus	BM639954 170006876	BU149265 AGENCOURT	AY407186 Mus muscu		AK080475 Mus muscu	BB16				Н	m	н	68	27	4155	5 UI-M	3069 6470	31 Pan t	9760 Bflo	0
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ALIGNMENTS

BG632919

GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster c CG4128: Fban6004128

'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazota; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilae; Drosophila.
I (bases I to 885)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Other ESTs: GH16126.Sprime
Contact: Stapleton, M. Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6494.
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a Xhol site followed by a run of 14 or BG632919.1 GI:13758409 EST. BG632919 BDGP RESULT 1 BG632919/c ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS TITLE JOURNAL COMMENT AUTHORS REFERENCE

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GATGAAGTTCGGCAGTTGGACCTACGACGGATTCCAGGT 451
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Drosophila melanogaster
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ilarity 98.5%;
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Matches 334; Conserv
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more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. hit genomic AE003511: arm:X [18792641,19136447] estimated-cyto:1873-1866: 04/10/2001 Plate: GH.161 row: C column: 2 High quality sequence stop: 784.
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                                                                                                                                                                                                                  /sex="male and female"
/dev stage="adult"
/lab_host="DHS - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="lorgan: head, Vector: pOT2; Site 1: EcoRI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
POT2. Plasmid cDNA library."
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                                                                                                                            1. .885
/organism="Drosophila melanogaster"
/mol_trpe="mRNA"
/db xref="taxon:7227"
/clone="GH16126"
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 74.6%;
Matches 534; Conservative
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Direct Submission

Submitted (102-JUN-1999) Genoscope - Centre National de Sequencage : Br 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone="BACR02C08"
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Pred. No. 8.2e-70;
1; Mismatches 4;
                                                                                                                                                                                                                                                    (fruit fly)
                                                                                                     fly), genomic survey sequence. AL058211
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/note="end : T7"
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Web: www.genoscope.ons.fr.

Web: www.genoscope.ons.fr.

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CNSOO6F9

Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR13K21 of RPCI-98 library from Drosophila melanogaster (fruit
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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al Similarity 99.1%;
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 ENTX cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosephila Genome Project (BDGP).
The BDGP is constructing these BACs. For further information please see http://www.fruitfly.org The BDGP Drosephila melanogaster genome using these BACs. For further information please see thtp://www.fruitfly.org The BDGP Drosephila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial Ecort diseation of Drosephila DNA provided by the BDGP from the Sognatic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACRAC Resource Center can be to the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of the County of
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/db_xref="taxon:7227"
/clone="BACR35F05"
/clone_lib="RPCI-98"
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Best Local Similarity 98.2%;
Matches 333; Conservative
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GH15518.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster con pot Drosophila melanogaster con GH15518 5 similar to CG4128: FBan0004128 ion channel' located on: 2L 30Dl-30El;: 04/10/2001, mRNA sequence A1292581
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I (bases 1 to 607)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.

BORP/HHMI Drosophila EST Project
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470 ACAGTGCTGATGAGGGCTTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTG
                                                                  GCTCGTGTCTATACGTTCCGCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003626: arm:2L [9617316,9882551]
estimated-cyto:30C7-30F4: 04/10/2001
Plates GH.155 row: B column: 6
High quality sequence stop: 521
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Other ESTs: GH15518.3prime
Contact: Stapleton, M.
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                                                                                                                                                                                                             AL530299 1201 bp mRNA linear EST 23-MAY-2003
AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.
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BP 191 91006 EVRY cedex - France
BF mail: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r For more information, about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full.length cDNA libraries and normalization Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12793792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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          GATGAAGTTCGGCAGTTGGACCTACGACGATTCCAGGT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD007YP05"
                                                                                                                                                                                                                                                                                                                                                      AL530299.2 GI:31068132
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59.8%;
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Homo sapiens
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Matches 503; Conserv
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TITLE
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LOCUS
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                                                                                                                /lab_host="DHS - alpha"
/clone lib="GH Drosophila melanogaster head pOT2"
/note="Corgan: head, Vector: pOT2; Site 1: EcoR1; Site 2:
XhoI; Sized fractionated CDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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Catarrhini; Hominidae; Homo.
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90134548 Single gene library Homo sapiens CDNA, mRNA sequence.
CD013901
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                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                      Score 265; DB 9; Length 60
Pred. No. 1.7e-53;
0; Mismatches 140; Indels
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PCR isolation and cloning of novel spli
                                                                  sex="male and female"
             xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug target genes
Unpublished (2003)
Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                        /dev_stage="adult"
/lab_host="DH5 - a
           db_xref="taxon:7
clone="GH15518"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:37777431
                                                                                                                                                                                                                                                                                                   11.5%;
Similarity 71.4%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 2296)
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/note="Vector: pDrive Cloning Vector; RT-PCR was perfor using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."
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0; Mismatches 330;
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                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                             CCCGGCAAACGTAACGAGATCTATTACAACTGCTGCCCGGAACCCTATATAGACATCACC 1530
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                              568 GIACTGAIATCIGCICTAGCCCIGCIGGGGIICCIGCIICCAGCAGAGAGAGAAG
                                                                             GAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCGAGTGGGAACTACTGGGTGTG
                                                                                                                            397 TCA------GACATATCTGAATATATCGTAAATGGAGAGTGGGACCTTGTAGGCGTT
                                                                                                                                                                                                                               448 cenddaaaaagagagaaattactargaargectdeaaggaaccgaaccttgargaca
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Functional annotation of a full-length mouse CDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/lab_host="DH10B (phage-resistant)"
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/clone_lib="Vector: pcWv-SFORT6; Site_1: Not1; Site_2: Sal1;
Cloned_un.directionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NGI-CGAP clone distribution information (clund through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI4228 row f. Column: 14
High quality sequence stop: 746.
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleost.
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                            Xenopus laevis cDNA clone
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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Pred. No. 3.8e-46;
0; Mismatches 268; Indels
                                                                                                                                                                                          linear
                                                                                                                                                                                             mRNA
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/organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                     922 bp
AGENCOURT 10492745 NICHD XGC_OO1
IMAGE:6642638 5', mRNA sequence.
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/db_xref="taxon:8355"
/clone="IMAGE:6642638"
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                    1713 AATGCCGGCTACTTC 1727
                                                                CATCCCGTCCACCTC 1140
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Matches 415; Conserv
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S Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kouno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Miramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp,
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RSPRTHTMPAMVRRVFLDIVPRLLFMKRPSVVKDNCRRLIBSMHKMANAPRFWPEPES
EPGILGDICNQGLSPAPTFCNRMDTAVETQPTCRSPSHKVPDLKTSEVEKASPCPSPG
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TYNTRKYECCAEIYPDITYAFIIRRLPLFYTINLIIPCLLISCLTVLVFYLPSECGEK
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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TRAVBGVQYIADHLKAEDTDFSVKEDWKXVAMVIDRIFLWMFIIVCLLGTVGLFLPPM
LAGANI"
                                                  Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 (b1)-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2940)
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RLFSGYNKWSRPVANISDVVLVRFGLSIAQLIDVDEKNOMMTTNVWVKOEWHDYKLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                          FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /noce="unnamed protein product; cholinergic recennication; alpha polypeptide 4 (MGD|MGI:87888, GB|NM_015730, evidence: BLASIN, 99%, match=1946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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/db_xref="MG1:3398424"
/db_xref="taxon:10090"
/clone="9330165116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/db_xref="GI:26329799"
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Score 232.6; DB 11; Length Pred. No. 2.4e-45; 0; Mismatches 344; Indels

10.1%; 56.6%;

Query Match 10.1 Best Local Similarity 56.6 Matches 452; Conservative

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1288
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RLESCYNKWSREVANISDVULVREGISIAQLIDVDEKNOMMTINVWKQEWHDYKLEN
DPGDYENVTSIRIPSELIWRPDIVLYNNADGDFAVTHLITKAHLFYDGRVQWTPPAJYK
SSCSIDVTFRPPDQQNCTMKFGSWTYDYAKIDLVSWHSRYDDLFBWSGEWNIVDAVG
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SCHPPNSGAPVLIKARSLSVQHYSSQEABEGSIRCRSRJQYCVSQDGABGITESPAL
TRAVEGVQYIADHLKAEDTDFSVKEDWKYVAMVIDRIFLMMFIIVCLLGTVGLLEPPN
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                                                                                                                                                                                                                                                                                                                                                                                                           /protein id="BAC38788.1"
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/translation="MEIGGSGAPPPLLLLPLLLLGTGLLPASSHIETRAHAEERLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1049 ATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGGGTAAAACTGGAGTGGAACG 1108
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                                                              /tissue type="hippocampus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                           receptor
                                                                                                                                                                                                               /note="unnamed protein product; cholinergic recenication; alpha polypeptide 4 (MGD|MGI:87888, GB|NM_015730, evidence: BLASIN, 99%, match=1946)
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/clone="C630019Ml8"
                                                                                                                                 /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yoneda,Y., Inshikawa,T., Ozawa,M., Ohara,E., Warahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Oxzaki,Y., Muramatsu,M., Inoue,Y., Kira,A and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer
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Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Stehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exploration Research
                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length bDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details
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/db_xref="MGI:2417536"
/db_xref="taxon:10090"
igh-efficiency full-length cDNA cloning
eth. Enzymol. 303, 19-44 (1999)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
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/clone="IMAGE:683671"
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/clone=lib="mbry ol 13:5,14:5,16.5,17.5dpc"
/clone lib="mbry ol 15:70"
/note="Organ: Brain; Vector: pYx-Asc; Site_l: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel: First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not! and then cloned
directionally into pXx-Asc vector. The library tag
sequence late adaptor, digested with Not! and the polyA tail
is ACGGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                         GIGIACIGALIGCCICCAIGGCCTIGCICGGAIICACCCIGCCGCCAGAIICGGGIGAAA 1648
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
Seq primer: pXx-5.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
742 CCTACGCCTTCATCATCCGCCGACTGCTCTTCTACACCATCAACCTTATCATCCCGT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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UL-M-FYO-cds-b-06-0-UI.x1 NIH_BMAP_FYO Mus musculus IMAGE:6833671 5', mRNA sequence.
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/mol_type="mRNA"
/strain="C57BL/6"
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Length 833;

9.9%; Score 228.8; DB 14; 57.5%; Pred. No. 1.4e-44;

Query Match Best Local Similarity

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1 (bases 1 to 1434)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, N. A.,

Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                 1042 ATTATCGATGTGGACGAGAAAAATCAATTGCTAGTCACTAATGTGTGGTTAAAAACTGGAG
                                                                                                                                                                                                                                                                                                                                          1102 TGGAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGA
                                                                982 CGTCCCGTTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTTAATGCAA
                                                                                                                             1 deccadradocadrarordadarorderocrostoceorradocaradocada
                                                                                                                                                                                                                                                                         61 crcarrdardrandanahanccagardangangangangrangrangranggangang
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       Gaps
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       3;
       Indels
Mismatches
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Conservative
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1712

796

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1113 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGCCGCA 1172
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                                                                                                                                                                                                                                                                                                                                                      DNA linear GSS 15-DEC-2003
Pan troglodytes CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence, genemic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACGAGAAAAATCAATTGCTAGTCACTAATGTGTGTTAAAACTGGAGTGGAACGACAT 1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan. 1 (Dases 1 to 1436)
11 (Dases 1 to 1436)
12 (Add, M.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu.F., Murphy, B., Reriaira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M.D. and Cargill, R. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms, M. Addms
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
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677 GCTCATCTCCTTCCTCACTGTGCTCGTCTTCTACCTGCCCTCCGACTGCGGTGAGAAGGT
                                                          1653 ATCGCTGGGTGTTACCATCTTGCTCTCGCTGACCGTGTTTCTGAATATGGTTGCCGAGAC
                                                                                                              737 gacccidideairircigiceiereeeereaceargiirereergaagaacacidagae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Pred. No. 6.7e-43;
0; Mismatches 357;
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Science 302 (5652), 1960-1963 (2003)
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/mol_type="genomic DNA"
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Pan troglodytes
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ORGANISM
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VERSION
KEYWORDS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                        Then, Lab. (bases 1 to 1436)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 CAAGCTGAAGTGGAACCCCTCTGACTATGGTGGGGGAGAGTTCATGCGTGTCCCTGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTACCAGACGAACGTGGTGCGGAACAACGGCTCGTGTCTATACGTTCCGCCGGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 egargaagraaaccagarcargaagaccaaccrefiegcreaagcaaarcregaargacra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1113 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATAACGCCGCA
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.larity 56.1%; Pred. No. 1.1e-43;
Conservative 0; Mismatches 346; Indels 3;
                           Science 302 (5652), 1960-1963 (2003)
14671302
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CHRNA3"
/locus_tag="HCM1369"
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand CDNA synthesis was primed with oligo-dr primer containing a Not I site. Doubbe strand CDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                         /tissue_type="whole brain"
/dev_stage="embryo12.5dpc"
/lab_host="bH10B (TI phage resistant)"
/clone_lib="NH10B (TI phage resistant)"
/note="Organ: Brain; Vector: pXx-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agargee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 219.6; DB 13;
Pred. No. 2.3e-42;
0; Mismatches 299;
                                            clone="IMAGE:6400763"
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Best Local Similarity 57.78
Marches 412; Conservative
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UI-M-FIO-byx-p-12-0-UI.rl NIH BMAP_FIO Mus musculus cDNA clone
IMAGE:6400763 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Irsue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi, Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/.
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/strain="C57BL/6"
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                          Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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                                                                                             AY406232 13-DEC.
Mus musculus CHRNA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Pred. No. 3.5e-42;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

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7, 2004, 11:09:28 ; Search time 66.2366 Seconds (without alignments) 3284.615 Million cell updates/sec

US-09-303-232-2

4043 Perfect score:

1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A Geneseq 29Jan04:* Database

geneseqp1980s: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES Res

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ALIGNMENTS

AAY50814 standard; protein; 770 AA. 17-FEB-2000 (first entry) AAY50814; RESULT 1
AAY50814
ID AAY5
XX

Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR. D. melanogaster acetyl-choline receptor protein from clone Da7.

Drosophila melanogaster

DE19819829-A1

11-NOV-1999.

98DE-01019829. 04-MAY-1998; 98DE-01019829 04-MAY-1998;

(FARB) BAYER AG.

Schulte T; Adamczewski M, Oellers N,

2000-014207/02. WPI; 2000-014207/ N-PSDB; AAZ24475. New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Example la; Page 12-14; 26pp; German.

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Drosophila melanogaster

Sequence 770 AA;

98DE-01019829 98DE-01019829

04-MAY-1998; 04-MAY-1998;

11-NOV-1999

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Query Match
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Marches 770; Conservative
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Best Local Similarity 70.0%
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SMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVA 305
                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity 97.4
Matches 297; Conservative
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                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL14485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 327 AA;
                                                                                                                                                                                                                                                                                                                          pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                  WO200171042-A2
                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                             Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
 246
                                          306
                                                                                   363
                                                                                                                                                 725
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                                                                                                                                                                                                                                               ABB70382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel nucleic acid (NA) encoding a nicotinic acety-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransmission. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (1) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence represents an acetyl-choline receptor isolated from Heliothus virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISSYVINGEWELLGVPGKRNEIYYNCCPEPYIDITFALIIRRRTLYYFFNLIIPCVLIA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                                                                                                          Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR.
                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
                                                                                                   virescens acetyl-choline receptor protein from clone Hva7-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.8%; Score 1609; DB 3; 60.8%; Pred. No. 1.1e-138; ive 57; Mismatches 65;
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                                                                                                                                                                                                                                                                                                                                                                       Example la; Page 22-23; 26pp; German.
                                                                                                                                                                                                                                                                                      Schulte
                                    AAY50816 standard; protein; 501 AA.
                                                                                                                                                                                                                      98DE-01019829
                                                                                                                                                                                                                                            98DE-01019829
                                                                                                                                                                                                                                                                                     Oellers N,
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                          2000-014207/02.
                                                                                                                                                       Heliothis virescens.
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Best Local Similarity
Matches 319; Consery
                                                                                                                                                                                                                                                               (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ24477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 501 AA;
                                                                                                                        Acetyl-choline
                                                                                                                                                                                                                                                                                    Adamczewski M,
                                                                                                                                                                           DE19819829-A1.
                                                                                                                                                                                                                     04-MAY-1998;
                                                                              17-FEB-2000
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                                                         AAY50816
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617
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                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                               SSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRK---TIMMANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
-WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS
                                                                                                      SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG-----GTLPHNPAFYRTV
                                                                                                                                                                                                                673 YGQG-----DDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 37938; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                             DECNDIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 8.3e-129;
4; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB70382 standard; protein; 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-0191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.1%;
97.4%;
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Sequence 311 AA;

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                                                                                                                                                    121 ITQQPTNIRLCARKRQRLRRRRRRRPATPNETDIKKQQQLSMPPFKTRKSTDTYSTPAAI 180
                                                            HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA 120
                                                                                           HSN11ASEÓHNSQQOEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therspettics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16179-ABL30511), expressed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic form at directly from WIPPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                         241 LFRRIAASTIAFISYLGSFAAQLKNSSSSSS-SSNSSNNSSTQILNGLNKHSWIFLLIYL
                   MKNAQLKLTEVDDDELWLAVRLAHCSSNISSSSSTRTTSSNKRHNQQLTTLQPRSLSTKH
                                                                                                                            TTQQPTNIRLCARKRQRLRRRRRRRRRPATPNETDIKKQQQLSMPPFKTRKSTDTYSTPAAT
 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
                                                                                                                                                                                       TSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLHVLQVLLVSLQQWQLHVQQRSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO 17841; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 17841
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                                                                                                                                                                                                                                                                                                                                                                                                                            ABB63683 standard; protein; 311 AA.
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11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
N-PSDB; ABL07786.
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                                                                                                                                                                                                                                                                                                                                               NLSAK 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
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                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated neuronal alpha-bungaro-toxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The alphal subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarotoxin binding protein (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in
                                                                                                                   79 DEKNOLLITNIWLKLEWNDMNLRWNSSEFGGVRDLRIPPHRLWKPDVLMYNSADEGFDGT
                                                                                                                                                                              139 YATNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDE
                                                                                                                                                                                                                          199 AGGDISSFIINGEWDLLGVPGKRNEIYYNCCPEPYIDITFAILIRRKTLYYFFNLIVPCV
                                                   295 LLIY----LNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
                                                                    DEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGT
                                                                                                                                                        YQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDE
                                                                                                                                                                                                           TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPCV
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
                                                                                                                                                                                                                                                               581
                           3
Length 311;
                                                                                                                                                                                                                                                                            LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuronal alpha-bungarotoxin binding protein alphal subunit.
                           Indels
  DB 4;
 34.8%; Score 1407.5; DB 4
88.6%; Pred. No. 1.8e-120;
                           18; Mismatches
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/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23. .502 ___/label= Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ligand binding; ion channel
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-118297/11.
               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lindstrom JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-1989;
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                           257;
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                                                                                                       352
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    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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                 Local
                            Matches
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recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alphal and alpha2 submits can also be used to produce submit peptides for use as immunogens for preparing antibodies to permit affinity purification of subtypes and their histological location
                                                                                                                                                                                                  295 ILIYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV 351
                                                                                                                                                                                                                                                                                     531
                                                                                                                                                                                                                                                                                                                                                                                                                           242
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                                                                                                                                                                                                                                                                                                                            YQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDE 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 IVGLSVVVTVIVLQYHHHDPDGGKMPKMTRVILLNWCAWFLRMKRPG-----EDKVRPAC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           615 DISSERKHQILSDVELKERSSKSLL-ANVLDIDDDFRH----NCRPMTPGGTLPHNPAFY 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECND 729
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                                                                                                                                                                                                                                                                                                                                               TGGDISSYVINGEWELLGVPGKRNEIYYNCCPEPYIDITFALLIRRTLYYFFNLIIPCV
                                                                                                                                                                                                                                                                                                                                                                                                         --ADISGYISNGEWDLVGIPGKRIESFYECCKEPYPDIIFIVIMRRRILYYGLNLLIPCV
                                                                                                                                                                                                                          ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCS
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 QHKQRRCS--LSSMEMNTVSGQQCSNGNMLYI--GFRGLDGVHCTPTTDSGVI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIASMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVARTMPATSDAVPL----
                                                                                                                                                                           75;
                                                                                                                                          29.2%; Score 1179.5; DB 2; Length 502; 45.7%; Pred. No. 3.7e-99; tive 80; Mismatches 127; Indels 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    730 IANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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                                                                                                                                                        Similarity
                                                                                                             Sequence 502 AA;
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Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                        Rat Protein Q05941, SEQ ID NO 3169.
                   standard; protein; 502 AA
                                                                                                                                                                                               14-AUG-2001; 2001US-0312147P.
                                                                                                                                                                             14-AUG-2002; 2002WO-US025765
                                                       (first entry)
                                                                                                                     Rattus norvegicus
                                                                                                                                        WO2003016475-A2.
                                                       29-JAN-2004
                                                                                                                                                          27-FEB-2003
                   ADE57308
                                    ADE57308;
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10; 353

Gaps

85;

Indels

Matches 238; Conservative

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68

Local Similarity

413 127 473

297 IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 354 KNOLLVINVWLKLEWNDMNLRWNISDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 185 ADISSYIPNGEWDLMGIPGKRNEKFYECCKEPYPDVTYTVTWTRRRTLYYGLNLLIPCVLI

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474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRILYYFFNLIIPCVLI

414 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG

67

184 533 244 245 SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVABIMPATSDSVPLIAQYFASTMIIV 304

534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-

--WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP

305 GLSVVVIVIVLRYHHHDPDGGKMPKWTRIILLNWCAWFLRMKRPGEDKVRPACQHKPR-

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or human polymucleotides or applying the propersents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the profice of a method for identifying a compound useful in treating activity in an animal of one or more of the polypeptides given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                       invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                       New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 502;
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                                                                                                                                         Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page; 1017pp; English.
                                                                                                                                      Befort K,
26-NOV-2001; 2001US-0333347P.
                                                     HOSPITAL
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                                                                                                                                   D'urso
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                                                                                                                                                                                                                                                                    composition
                                                                                                                                                                                                                    GENBANK; Q05941
                                                  (GEHO ) GEN HC
(FARB ) BAYER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a paramaceutical composition, a method for identifying a compound useful in the cativity in an animal of one or more of the polypeptides given in the cativity in an animal of one or more of the polypeptides given in the cativity in an animal commonsition and a compound useful in treating composition and a percent of the polypeptides given in the cativity in an animal commonsition commission the or more
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                             ----PPTSNGNLLY--IGFRGL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                         Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                             393 EGMHCAPTPDSGVVCGRLACSPTHDEHLMHGAHPSDGDPDLAKILEEVRYIANRNRCQDE
CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTV
                                                           ---GDDGSI-GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDE
                                                                                                                                         SEVICSEWKFAACVVDPLCLMAFSVFTICTIGILMSAPNFV 494
                                                                                                                          CNDIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Costigan M;
                                                                                                                                                                                                                                                                                                                            Protein AAC33136, SEQ ID NO 12737
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                              -----LASVELSAGAG-
                                                                                                                                                                                                                                   ADD47049 standard; protein; 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D'urso D,
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therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                     68 KNQVLTTINIWLQMSWIDHYLQMNMSEYPGVKNVRFPDGQIWKPDILLYNSADERFDAIFH
                                                                                                                                                                                                                                                245 SALALLVFILPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 GLSVVVTVIVLRYHHDPDGGKMPKWTRIILLNWCAWFLRMKRPGEDKVRPACQHKPRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                  354 KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                                                                                                                                                                                                                      TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                                                                                                                                                                                             128 TNVLVNASGHCQYLPPGIFKSSCYIDVRWPPFDVQQCKLKFGSWSYGGWSLDLQMQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                              GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
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                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAFTMPATSDAVPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding protein alpha 2; cholinergic;
                                                                                                                                                                                       85;
                                                                                                                                                   Length 502;
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                                                                                                                                                                                       Indels
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1.3e-98;
ches 119; I
                                                                                                                                                                      Pred. No. 1.3e-80; Mismatches
                                                                                                                                                   29.0%; Score 1173.5; 45.6%; Pred. No. 1.3e
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/label= Mat_protein
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/label=_Sig_peptide
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                                                                                                                                                                                         Matches 238; Conservative
                                                                                                                                                                      Similarity
                                                                                                                   Sequence 502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-1997
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AAW44153
              The alphal subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of chick neutronal alpha-bungarotoxin binding protein (ABBP) were deduced from neuly isolated DNA molecules (AAT59196-97) obtd. from an 18-day chick embryo cDNA library. ABBP subunits can be produced in recombinant host cells, pref. a bacterium, and used in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact ABBP subtypes. The ABBP alphal as immunogens for preparing antibodies to produce subunit peptides for use subtypes and their histological location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 NGLNKHSWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 QPSNGNMIYSYHTMENPCCPQNNDLGSKSGKITCPLSED--NEHVQKKALMDTIPVIVKI 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFF 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 YFASIMVIVGLSVVVTVLVLQFHHHDPQAGKMPRWVRVILLLNWCAWFLRMKKFGENIKPL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 ILEFPTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPH 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---H 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               711 LKBIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGLCLWASLFLSFF-----KVSQQGESQRRLYRDLLRNYNRLERPVMNDSQPIVVELQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----WIRIVFLCWLPWILRMSRPG---RPL
                                                                                                                                                               New isolated neuronal alpha-bungaro-toxin-binding protein DNA - us screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCKY-----SYPKHHPSLKNTEM------NVL-
                                                                                                                                                                                                                                                                                                                                                                                                                                   28.9%; Score 1168; DB 2; 44.2%; Pred. No. 4.4e-98;
                                                                INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                        Example; Fig 3A-B; 18pp; English
           89US-00413947
                                    89US-00413947
                                                                                           Schoepfer RD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 NPAFYRTVYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                       WPI; 1997-118297/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 238; Conserv
                                                                                                                                    N-PSDB; AAT59197
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 511 AA;
                                                                                             Lindstrom JM,
           28-SEP-1989;
                                     28-SEP-1989;
                                                                 (SALK ) SALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
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The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit ombinations with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subtypes.
than drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuronal nicotinic acetylcholine receptor subunits and DNA - also transformed cells useful for screening cpds. which modulate activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             should lead to the identification and design of compounds that are expable of very specific interaction with one or more receptor subtracts. The resulting drugs should exhibit fewer unwanted side effects that identified e.g. screening with cells that express a variety of subt
                                                                                                                                                                                                                     Human, neuronal nicotinic acetylcholine receptor; alpha-7 subunit; brain tissue; screening; NAChR; antibody.
                                                                                                                                                                  Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= cytoplasmic_loop
                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
AAW44153 standard; protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 80-81; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Harpold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= TMD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162. .487
|abel= TMD4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= TMD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-303024/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the receptor.
                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9420617-A2
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                                                                                                             14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-1994
                                                        AAW44153;
                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
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Score 1159.5; DB 2; Length 502; Pred. No. 2.6e-97;

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                                                                                                                                                                                                                                                                                                                                                    -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAXILEEVRYIANRFRC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding nicotinic acetyl:choline receptor sub-units - used in screening to determine the effect of drugs on the receptor.
                                                                                                                                                                                                                         304
                                            67
                                                                               TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---
                                                                                                                                                                                                               305 GLSVVVTVIVLOYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACOHKORR
                                                                                                                                                                                                                                                                                                                                     ---HTCIKSSTEYELGLILKEIRFITDQLRK
                       IYLNLSAK----VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                  KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                            TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                         GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                  534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                               WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                          CSDTSSERKHQ1LSDVELKERSSKSLLANVLD1DDDFRH----NCRPMTPGGTLPHNPAF
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
  91;
                                                                                                                                                                                                                                                                                                               CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP-
                                                                                                                                                                                                                                                                                                                                                                                            Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
  Indels
                                                                                                                                                                                                                                                                                                                                                                                DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII
  Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 73-74; 108pp; English
                                                                                                                                                                                                                                                                                                                                     669 YRTVYGOGDDGSIGPIGSTRMPDAVTH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SIBI-) SIBIA NEUROSCIENCES INC
82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-00484722
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
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The alpha-7 subunit (AAW09025) of the human neuronal nicotinic caetylcholine receptor (nAcNR) can be expressed in transformed host cells carrying alpha-7 subunit DNA (see also AAT48299). Host cells, esp. mammalian cells or amphibian cocytes, expressing the recombinant alpha-7 subunit, opt. in combination with other recombinant alpha and/or beta subunit, see also AAW09018-24, AAW09026-27), can be used to examine the function of human AChR and to identify cpds. that modulate its activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVABIMPATSDSVPLIAQYFASTMIIV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAXILLEEVRYIANRFRC 449
                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                         --HTCIKSSTEYELGLILKEIRFITDQLRK
                                                                                                                                                                                                                                                                                   297 IYLNLSAK----VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE
                                                                                                                                                                                                                                                                                                                                                            KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ
                                                                                                                                                                                                                                                                                                                                                                                             KNOVLTTNIWLOMSWIDHYLOWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFH
                                                                                                                                                                                                                                                                                                                                                                                                                                     TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRRTLYYGLNLLIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; tumourigenesis; identification; cancer; cytostatic; neotroprotective; antiinflammatory; immunosuppressive; immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalmic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stronal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder.
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                              91;
                                                                                                                                                                                                          Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 450 QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGLLMSAPNFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII
                                                                                                                                                                                                      28.7%; Score 1159.5; DB 2; 45.1%; Pred. No. 2.6e-97; ive 82; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO2145 protein sequence SEQ ID NO:77.
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                                                                                                                                                                                                                                            237; Conservative
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                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                     Sequence 502 AA;
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Nicotinic acetylcholine receptor; nAChR; human; acetylcholine binding protein; AChBP; mollusc; ligand-binding protein; ligand-gated ion channel; crystal; drug design; protein co-oxdinate data; schizophrenia; Alzheimer's disease; nicotine addiction; Tourette's syndrome; therapy; nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DSGVV----CGRMACSPTHDEHLLHGGQPPBGDPDLAKILEEVRYIANRFRC 449
                                                                             SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Water-soluble ligand-binding proteins derived from molluscs and analogs of ligand-gated ion channels, useful in drug screening assay, where the drugs identified can be used in the treatment of Alzheimer's disease or
                                                                                                                                                                                                                                                                                                 CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF
                                                                                                                                                                                                                                    305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGGDKVRP-ACQHKQRR
                                                                                                                                                                                                                                                                                                                                                                                                                              669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK
                                                                                                                                                                                                                                                                                                                                                          CSLASVE----MSAVAPPPASNGNLLY----IGFRGLDGVHCVP-TP
                                           534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSADNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
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/note= "conserved ligand-binding region,
and Tyr173 are essential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "conserved ligand-binding region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Tyr115 are essential"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotinic acetylcholine receptor alpha7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TEWE-) STICHTING TECH WETENSCHAPPEN.
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2000EP-00203810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619, PRO171, PRO8099, PRO8019, PRO1801, PRO8090, PRO8019, PRO1801, PRO80190, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO1801, PRO20191, PRO1801, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, PRO20190, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRTLYYGLNLLIPCVLI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thirty PRO polynucleotides encoding PRO polypeptides, useful in the treatment, diagnosis and prevention of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillan KJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 61; Fig 58; 286pp; English.
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99US-0141037P.
99US-0143048P.
99US-0145698P.
99WO-US028313.
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Wood WI;
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les 237; Conservative
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N-PSDB; AAC58395.
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WO200053755-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashkenazi AJ,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-2000;
                                                                                                                            06-JAN-2000;
                                                                                                                                                                                                                                                                                          07-JUL-1999;
                                                                                                                                                                                                                                                                                                                     26-JUL-1999;
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Matches
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residues Tyr210,

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QQ

8

residues Trp108 residues Trp171 Human, alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance.

WO200073431-A2. Homo sapiens.

99US-0136174P. 2000WO-US011862.

25-MAY-2000;

07-DEC-2000

gated ion channel.

Wild-type human alpha7 ligand

(first entry)

14-MAR-2001

conserved throughout the various nAChR alpha subunit or induced infoculing cestal throughout the various nAChR alpha subunits and which are escential for ligand binding. The invention relates to water-soluble ligand-binding proteins derived from molluscs, especially acetylcholine-binding proteins (AChBPs) and analogues of ligand-gated ion channels, their crystals, and their use for screening ligands of ligand-gated ion channels. Coming multimers and are amenable to crystallization. The crystal spread can be used to generate 3D models of the extracellular ligand-binding domain of ligand-gated ion channels and thus for screening of drugs that act on these ion channels. Chinneric proteins are provided that are capable of binding a ligand of a ligand-gated receptor, and comprise at least the amino acids of the AChBP captering and comprising amino acids determining binding to the ligand. AChBP, and also comprising amino acids determining binding to the ligand. Corresponding amino acids determining binding to the ligand. Corresponding amino acids, and preferably entire stretches have been substituted. New drugs can be developed that selectively intervene in neuronal signalling pathways, especially where the ligand-gated ion channel is the nAChR, and the related disorder is fourette's syndrome, channel is the nAChR, and the related disorder is fourette's syndrome, and prefered disorder is fourette's syndrome.

502 AA;

12; 353 413 473 184 533 244 581 612 668 304 VRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK 723 -----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449 67 TWVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV IYLNLSAK----VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLOLSFGLTLMQIIDVDE TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG -WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP 305 GLSVVVTVIVLQYHHDDPDGGKMPKWTRVILLINWCAWFLRMKRPGEDKVRP-ACQHKQRR CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRRTLYYGLNLLIPCVLI 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-----Gaps 91; DB 4; Length 502; CSLASVE----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768 QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494 Indels 115; ; Score 1159.5; DB; ; Pred. No. 2.6e-97; 82; Mismatches 115 28.7%; 45.1%; Matches 237; Conservative Local Similarity 297 æ 89 128 474 185 364 450 414 699 724 Query Match 582 613 402 ð g g ð В à q d à q à a à a ð 셤 ò à

The present sequence is wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chineric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH. 353 999 413 473 244 304 ---HTCIKSSTEYELGLILKEIRFITDQLRK 723 581 305 GLSVVVTVIVLQYHHDDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR CSDISSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE---297 IYLNLSAK----VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 8 VWLALAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTVYFSLSLLQIMDVDE 245 SALALLVFLLPADSGEKISLGITVLLSLTVFWLLVAEIMPATSDSVPLIAQYFASTMIIV KNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ TNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFALIIRRRTLYYFFNLIIPCVLI --WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP Gaps 91; DB 4; Length 502; 364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP-534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-Indels 28.7%; Score 1159.5; DB 4; 45.1%; Pred. No. 2.6e-97; ive 82; Mismatches 115; Disclosure; Page 61-63; 77pp; English 669 YRTVYGOGDDGSIGPIGSTRMPDAVTH-ΨP. Berkenpas (PHAA) PHARMACIA & UPJOHN CO. Local Similarity 45.1 tes 237; Conservative Wolfe ML, WPI; 2001-061524/07. N-PSDB; AAC90380 Sequence 502 AA; 27-MAY-1999; Groppi VE, 354 89 414 128 474 582 613 Query Match Best Loca Matches g qq g à a ò 셤 à d δ à à à

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AAB50012 standard; protein; 502 AA

AAB50012;

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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (nNAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human NNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human encoded by the transfected nucleic acid. This sequence represents the alpha 7 subunit of the human nNAChR
---DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to NACHR.
                                                                                                                                                                                                                                              an; neuronal nicotinic acetylcholine receptor; nNAChR; receptor; flux; alpha 7 subunit.
                                                                                                                                                                                                                  Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
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                                            QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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                           DDECNDIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHII
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TNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQB-
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                                                                           ThrSerCysProThrAlaThrTyrWetGlnCysArgAlaSerAspAsnGluPheSerIle
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BAYER AD DZOSOPALIA melanogaster

D 25-JAN-2000;

PD 25-JAN-2000

PF 26-JAN-2000

PF 26-JAN-1999 DE 199918159

PR 04-MAY-1999 DE 19819829.9

PI MARTIN ADANUTSUBUSUKI, NADJA ERASU, THOMAS SCHULTE PC CI2NI/69, A01K67/033, CO7K14/705, CO7K16/28, C12NI/21, C12NIS/10, PC C12Q1/68,

PC G01N33/15.G01N32262///
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                                                         E58346.1 GI:13019345
JP 2000023680-A/1.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopteraygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                         Martin, A., Nadja, E. and Thomas, S.
Nucleic acid encoding insect actyl choline receptor subunit
Patent: JP 2000023680-A 1 25-JAN-2000;
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/organism="Drosophila melanogaster"
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Mismatches:
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/note="unnamed protein
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                                          TyrTyrPhePheAsnLeuilelleProCysValLeuileAlaSerMetAlaLeuLeuGly 540
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Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: BP 0962528-A 1 08-DEC-1999;
BAYER AG (DE)
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                                                            PheThrLeuProProAspSerGlyGluLysLeuSerLeuGlyValThrIleLeuLeuSer
                                                                                                                         1992 TICACCCTGCCGCAGATICGGGTGAAAATTATCGCTGGGTGTTACCATCTTGCTCTCG
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
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coetton/Qualifiers	Score: 4014.50 Matches: 770 Percent Similarity: 95.42\$ Conservative: 0 Best Local Similarity: 95.42\$ Mismatches: 0 Query Match: 99.30\$ Indels: 37 DB: 3 Gaps: 1 US-09-303-232-2 (1-770) x AF27277B (1-2907)	Qy 1 MetLysasnaladlinleulysLeuThrGluValaspaspaspGluLeuTrpLeuAlaVal 20	21 ArgLeuAlaHisCysSetSerAsnPheSerSerSerSerThrArgThrThrSerSer 	Qy 41 AsnGlnArgHisAsnGlnGlnLeuThrThrLeuGlnProArgSerLeuSerThrLysHis 60 1	61 HisSerAsnileAlaSerGluGlnHisAsnSerClnGlnGlnGlnGluProAlaSerIySASP 8	81 GluaspValalaasnHisGlyAxgSerAsnAspGlnGlnThrHisLeuGlnGlnLeuAsp 	101 SerSerAsnMetLeuSerProLysThrAlaAlaAlaAhaThrAlaAlaGlyAspGluAla 	121	141 ArgarglysarglysproalaThrProAsnGluThrAspIleLysLysGlnGlnGlnLeu 	2y 161 SerMetProProPheLysThrArgLysSerThrAspThrTyrSerThrProAlaalaThr 180	2y 181 ThrSerCysProThrAlaThrTyrMetGlnCysArgAlaSerAspAsnGluPheSerIle 200	2y 201 ProlleSerArgHisAspArgValSerThrAlaThrPheAlaTrpValLeuHisValLeu 220	2y 221 GlnValLeuLeuValSerLeuGlnGlnTrpGlnLeuHisValGlnArgSerValLeu 240	241 LeuPheArgArg11eAlaAlaSerThr11eAlaPhe11eSerTyrLeuGlySerPheAla 260	261 AlaGinLeuLysAsnSerSerSerSerSerSerSerSerAsnSerSerAsnasnSerSer	281 ThrGinileLeuasnGlyLeuAsnLysHisSerTrpIlePheLeuLeuIleTyrLeuasn 300	301 LeuSerAlaLygValCysLeuAlaGlyTyrHisGluLysArgLeuLeuHisAspLeuLeu 320	**************************************
	la melanogaster" 17.	7	czalpha-34E" n channel; neurotransmitter transmembran art=1	/product="micotinic acetylcholine receptor Dalpha5 subunit" /protein_id="AAM13390.1" Db	/GD_XXE1="C1": 2012;2840" /CFTATE 1 at 1 on="WRONAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRH NQQLTTLQPRSLSTKHHSN1ASEQHNSQQQEPASKDEDVANHGRSNDQOTHLQQLDSS NMLSPKTAAAATAGDERATTQOFTNT ELCARREQERRERRERRERRERERED KVQQQL SMDDERTTLQPRSLATAGDERTTTQOFTNT STATTGOFTNT STATTGOFTNT DOTHER STATTGOFTN ST	ONE CTAINNESS IT SET FAR AS ITSCHING SELECTION OF THE SERVING	ANTERNATION OF THE TOTAL TOTAL OF THE TOTAL	DODREHNCRPATROTEPTIVESDISSERRHQILSDVELKERSSKELLANVIDI DODREHNCRPATROGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSST EYELGIILKEIRFITDQLRKDDECNDIANDWRFAAMVVDRLCLIIFTWFAILATIAVL LSAPHIIVS" DD	3/3 /gene="nAcRalpha-34E" /note="compared to B allele" /replace="a" Db	/gene="nAcRalpha-34E" /note="results in phenylalanine to isoleucine substitution; compared to B allele" Db	oha-34E" s in threonine to isoleucine substituti	/replace="t"	/ / / / / / / / / / / / / / / / / / /	arbing 372 Fried asparagine and Ballele"	alpha-14E" lts in serine, glycine, and asparagin compared to B allele"	aragine to serine substituti	/replace="g" Db	

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GPVVDGRLHBALSHTCLIASARSELALILKELRWITEQLKKEDBTSDITRDWKFAAMV
VDRLCII FTLFTIIATLAVLFSARFELALILKELRWITEQLKKEDBTSDITRDWKFAAMV
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/gene="nAcRalpha-18C"
/product="nicotinic acetylcholine
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Matches:
Conservative:
Mismatches:
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                                                                                                                           CAGATACTCTCCGACGTTGAGCTGAAAGAGGGCTCGTCGAAATCGCTGGTGGCCAACGTA
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                                   IleArgileValPheLeuCysTrpLeuProTrpIleLeuArgMetSerArgProGlyArg
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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| product="nicotinic acetylcholine receptor subunit
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Drosophila melanogaster (fruit fly)
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/organism="Drosophila
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740	:: ::	O. O. O. O. O. O. O. O. O. O. O. O. O. O	ORGANISM
532	12 LeulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLySLeu 551 	REFERENCE AUTHORS TITIE	ENCE THORS
552 860	SerLeuglyValThrIleLeuLeuSerLeuThrValPheLeuAsmMetValAlaGluThr 	C.	
572	MetProAlaThrSerAspAlaValProLeu	REFERENCE AUTHORS	SFERENCE AUTHORS
920		JTI	JOURNAL
196	ATGENCIACITICAL AND ACTIVITIES AND	FEATURES	RES source
582			
1040	GATACGCATGAAATGAGTGAATGGATAAGAGTAATATTCCTTTATTGGTTACCTTGCATA		CDS
595	LeuArgMetSerArgProGlyArgProLeuIleLeuGluPheProThrThrProCysSer 61		
615	2		
1157	TCGAGITCCTCCGCATCCGGCGAGAAGAAGCAACAGATCCAAAACGTTGAGCTCAAG		
632			
1214	4 GAGAGGICCTCCAAGTCICTGCTGGCCAATGTGCTCGATATAGACGATGATTTCCGA 1270	_	
652	AsnCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyrArgThr	ORIGIN	z
672	ValTyrGlyGlnGlyAspAspGlySerIleGlyProlleGlySerThr	Alignment	ment Sc
1328		Pred. No.: Score: Percent Si	No.:
688		Best]	Best Local S Ouery Match:
1388	GACG	DB:	
206		03-09	US-09-303-23
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1505	GAAACAAGCGACATTACGCGAGATTGGAAATTTGCTGCCATGGTCGTCGATCGTTGTG	δλ	31
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AF143846 3629 bp mRNA linear INV 27-WAY-1999 Heliothis virescens putative nicotinic acetylcholine receptor alpha AF143346 GI:4895004

LOCUS DEFINITION

AF143846

ACCESSION VERSION

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Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hespidoptera; Glossata; Ditrysia;
Noctucidea; Noctuidae; Heliothinae; Heliothis.
1 (Bases 1 to 3629)
Schulte, T., Oelleers, N. and Adamczewski, M.
Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Cezi
than to other insect nicotinic acetylcholine receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MGGRARRSHLAAPAGLLLLCLLMPRGARCGYHEKRLLHHLLDH
YWYLERPWYNESDPLQLSFGLTLMOTIDVDEKNQLLITNIWLKLEWNDMNLRWNTSDF
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DEDADISRDWKFAAMVVDRLCLIIFTLIATLATLAVLLSAPHINVS"
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Heliothis virescens (tobacco budworm)
Heliothis virescens
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735 LysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrMetPheAlaIle	LOCUS AX005612 DEFINITION Sequence 3 from Patent EP0962528. DEFINITION Sequence 3 from Patent EP0962528. ACCESSION AX009612. VERSION AX009612.1 GI:9996844 KEWORDS Heliothis virescens (tobacco budworm) CRGANISM Heliothis virescens (tobacco budworm) CRGANISM Heliothis virescens (tobacco budworm) NGGANISM Heliothis virescens (tobacco budworm) NGGANISM Heliothis Virescens (tobacco budworm) NGGANISM Heliothis Virescens (tobacco budworm) NGCANIGM Heliothis (tobacco budworm) NGCANIGM Heliothis (tobacco budworm) NGCANIGM Heliothis (tobacco budworm) NGCANIGM Heliothis (tobacco budworm) NGCANIGM Heliothis (tobacco budworm) NGCANIGM Heliothinae; Heliothis.	AUTHORS Adamczewski, M.D., Schulte, T.D. and Oellers, N.D. TITLE Nucleic acids encoding acetylcholin-receptor subunits from insects JOURNAL Patent: EP 0962528-A 3 08-DEC-1999; BAYER AG (DE) FRATURES Location/Qualifiers Source 1.3700	/ protein / protein / protein / protein / protein / protein / protein / protein / db_xref="NEI-996845" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-9968455" / db_xref="NEI-99684555" / db_xref="NEI-9968455555" / db_xref="NEI-9968455555" / db_xref="NEI-99684555555" / db_xref="NEI-99684555555" / db_xref="NEI-996845555555" / db_xref="NEI-996845555555" / db_xref="NEI-99684555555555" / db_xref="NEI-9968455555555555555555555555555555555555	Alignment Scores: 2.21e-125 Length: 3700 Pred. No.: 1850.00 Matches: 361 Scoret Similarity: 75.78% Conservative: 30 Best Local Similarity: 69.96% Mismatches: 49 Query Match: 65.76% Indels: 76 DB: 65.76% AX009612 (1-3700)	Oy 295 LeuLeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyrHisGluLysArg 314 Db 383 CTGCTGCTGCTGCTGCTGGGGGGGGGGGGGTGCGGGGAAGGGG 442 Oy 315 LeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGluArgProValLeuAsnGluSer 334 443 CTACTGCACCACACACACACACACGAGGGGGCCCTCTCACAGAGGGC 502 Oy 335 AspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIlelleAspValAspGluLys 354
683 AAACCAGACGTCCTTATGTACAACAGGGGGAAGGGTTCGACGGATATCCAACG 742 415 ASNVAlValArgASNAENGlySerCysLeuTyrValProProGlyllePheLysSer 434			ThrSerAspalaValProLeu	598 SerArgProGlyArgProLeuIleLeuGluPheProThrThrProCysSer	655 PrOMETTHEPROGLYGLYTHELEUPROHISASHPROALAPHETYRAGTHEVALTYEGLY 674 1532

QY 695 HisHisThrCysIleLysSerSerThrGluTyrGluLeuGlyLeuIleLeuLysGluIle 714 Db 1601 GCGCACAGTTGCTTCGGTGTCGACTCCCCTCATTCTGAGGGGTT 1654 QY 715 ArgPhelleThrAspGlnLeuArgLysAspAspGluCysAshAspIleAlaAsnAspTrp 734 Db 1655 AGAGTCATCACAGATCAGCAGACGACGACGACGACTTTTCGCGCGACTGG 1714 QY 735 LysPheAlaAlaAnaCAGATCAGCAGACGACGACGACATTTCGCGCGACTGG 1714 Db 1715 AAGTTCGCCCCATGGTCGTGCACAGACTGTGCCTTATTATCTTTACCTGTTCACAATC 1774 QY 755 LeuAlaThrIleAlaValLeuLeuSerAlaProHisIleIleValSer 770 Db 1775 ATGGCCACAGGTGGTGCTGTGCCGCCACACATCATGTTGTCG 1822 Db 1775 ATGGCCACAGACGCCGCCACACATCATGTCGTGG 1822	P 15	AUTHORN MATTIN, A., Nadja, E. and Thomas, S. TITLE Nucleic acid encoding insect actyl choline receptor subunit Patent: JP 2000023680-A 2 25-JAN-2000; BAYER AG COMMENT OS Heliothis virescens PD 25-JAN-2000 PF 26-APR-1999 JP 1999118159 PR 04-MAY-1999 DE 19819829.9 PI MARTIN ADAMUTSUEUSUKI, NADJA ERASU, THOMAS SCHULTE PC	PC GOIN33/15,GOIN33/50/(CI2N1/21,CI2R1:19),CI2N15/00,CI2N5/00 CC FH Key Location/Qualifiers FT CDS (335)(1822). Location/Qualifiers 1.3701 / Organism="Heliothis virescens" /mol type="genomic DNA" ORIGIN /db_xref="taxon:7102"	res: 2.21e-125 1850.00 arity: 75.78 milarity: 69.96\$ 6.76\$	US-09-303-232-2 (1-770) x E58347 (1-3701) QY 295 LeuLeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyrHisGluLysArg 314
375 TrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProProHisArgIleTrp 394 [111111111111111111111111111111111111	3232	H—4 01—H 5—0			635 SerLysSerLeuleuAlaAsnValleuAsplleAspAspAspPheArgHisAsnCysArg 654 [1481 TCCAAGTCGCTCCTAGCGAACGTGCTCGACATCGATCGACTTCGGCCAC 1531 655 ProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTytArgThrValTyrGly 674 [1532CCGCAAGCGAGCAGCGCGAATGCTGCCGATACTACAGG 1570 675 GlnGlyAspAspGlySerIleGlyProIleGlySerThrArgMetProAspAlaValThr 694 [1571 GGGGGTGAGGAGAGAGCGCGGG

	PheAlaileileileargargarghrLeuTyrTyrPhePheAsnLeuileileProcys 530 TTTACTATACAATTCGTCGCGTACATTATATTTTTTCAATTTAATCGTGCCATGT 112 ValLeuileAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLys 550 GTGCTAATCTCATCGATGGCCCTACTGGGCTTCACATTGCCGCGGATTCGGGCGAGAA 118 LeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGlu 570 CTGACGCTGGGGCTAACTACTATACATTAACAGTATTCTAAACCTTGCGCCGAG 124 ThrMetProAlaThrSerAspAlaValProLeu	1303 TTCATGGTCGCTCGTCGACAGAGTGGTCGTCAACTACCACCACCACA	CTAATTCTCAAAGAATTGCAATTTATTACGGCGCGATGCGCAAAGCTGACGACGACGGATGCCAAAGCTGACGACGAAGCGGATGCGCAATTTATTACGGCGCGGATGCGCAAAGCTGACGACGAAGCGGATGCAAGCTGACGACGAAGCGGATGCGATGGAAGCTGACGAAGCTGACGAAGCTGACGAAGCTTTATTATTATTATTATTATTATTATTATTTAT
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LSLTVFLNLVAESMPTTSDAVPLIGTYFNCIMFWVASSVVLTVVVLNYHRTADIHEM PPWIKSVFLOWLPWILRMGREGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDD DPRHTISGSGYALGSSASFGRPTTVEEHHTALGCNHKDLALLLKELGFITARMRKADD EAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHITUG" 793. 794 / Gene="nackalpha-30p" / note="results in glycine to asparagine substitution; / note="results in glycine to asparagine substitution; / note="results in glycine to asparagine substitution; / note="results" / Gene="nackalpha-30p" / Gene="nackalpha-30p" / note="results in glycine to serine substitution; compared to variant clone"	946ne="nAcRalpha-30D" / Jobe="results in asparagine to serine substitution; / Note="results in asparagine to serine substitution; compared to the sequence deposited in GenBank Accession / Number AE003626 and in variant clone" / Replace="a" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nAcRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D" / Johne="nacRalpha-30D"	2.56e-109 Length: 2023 1625.50 Matches: 320 70.44\$ Conservative: 47 61.42\$ Mismatches: 75 40.21\$ Mismatches: 75 40.21\$ Indels: 79 30) x AF321446 (1-2023) 1ePheLeuLeulleTyrLeuAsnLeuSeralalysValCysLeualaGlyTyr 31:	391 HishrgiloTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspGly 410 ***********************************
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/gene="nAcRalpha-30D"
/note="results in serine deletion; compared to variant
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                                                      to serine substitution;
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/note="compared to variant clone"
/replace="t"
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/note="results in asparagine
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BAELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
                                                                                                                                                                      2023 bp mRNA linear INV 29-APR-2002 inicotinic acetylcholine receptor Dalpha6 (nAcRalpha-30D) mRNA, complete cds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            пd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3a and 8b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MDSPLPASLSLFVLLIFLATIKESCQGPHEKRLLNHLLSTYNTL
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (Dases 1 to 2023)
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify and Mighly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="nAcRalpha-30D"
/note="results in isoleucine to methionine substitution;
compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grauso, M. and Sattelle, D.B.
Direct Submission
Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="results in asparagine to glycine substitution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="nicotinic acetylcholine receptor Dalpha6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .2023
Coganism="Drosophila melanogaster"
(mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAM13392.1"
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379. .1863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="30D1"
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[. .2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 2023)
suso, M. and Sattelle, D.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome="2"
                                                                                                                                                                                             Drosophila melanogaster
subunit variant type I (
alternatively spliced.
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                                                            . 694
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ORGANISM
                                                                                                                                     RESULT 10
AF321445
                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
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PUBMED
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AUTHORS
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CON SS SS SS SS SS SS SS SS SS SS SS SS SS	Direct Sub Submitted University KINGDOM L		EARVANESELLE KKEGLILQUIIDVDEKNQLLITUNALSLEWNDYNLEWNETEYGGYK DIRITPNKLWKEDVLMYNSADERDGTYHTSVVVKHGGSCLYVPPGTIFKSTCKMDITW PREDDQHCEMKFGSWTYDROLUSESEDGGDLSDFITNGRWYLLANFGKKUTIVYA CCPERYVDITFILQIRRRILYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL LSLIVYRLNIVAESMTTSDAVPLIGTYFROLINFWNASSVULTVVVLNYHRTRATITATIHEM PPWIKSYPLQWLPPILRMGRPGRKITRKTILLSNRWKELELKERSSKSLLANVLDIDD DFRHTISGSQTALGSSASFGRPTTVREHHTAGCHROHALLIKELGFITARWRKADD EABLIGDWKFAAMVUDRFCLIVFTLFTIIATVTVLLSAPHIIVQ" (Genne="NACFA")	mat_peptide //gene="nacaapua-300" /gene="nAcRalpha-300" /groduct="nicotinic acetylcholine receptor subunit Dalpha6" Alignment Scores: 3.89e-109 Length: 1665 Score: 1621.50 Matches: 320 Percent Similarity: 70.44\$ Conservative: 47 Best Local Similarity: 61.42\$ Mismatches: 75	40.11% Indels: 79 3 Gaps: 7 6) x DME554209 (1-1665) 1ePheLeuLeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyr	311 311 328	Qy 331 LeuAsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIleIleAsp 350 Db 188 GCCAATGAATCGGAGCCCCTGGAGGTTAAGTTCGGACTGACGCTGCAGCAGATCATCGAC 247 Qy 351 ValAspGluLySAsnGlnLeuLeuValThrAsnValTrpLeuLySLeuGluTrpAsnAsp 370 Db 248 GTGGACGAGAGAATCAGCTTCCATAACGAATCTTTGGCTTTCGTTGGAGTGGAACGAC 307
Db 943 GAAGATGGAGGGATCTTTCGATTTCATAACAAATGGCGAGTGGTACTTGCTTG		Db 1303 TTCATGGTCGCCTCGTCGGTGGTGCTGACAGTGGTGCTCAACTACCACCATCGCACA 1362	614 SerAspThrSerSerGluArgLysHisGlnIleLeuSerAspValGlu 1456ACAGGAAAACAATACTATTAAGCAATGGCATGAAGGAGTGGGAG 630 LeuLysGluArgSerSerLysSerLeuLeuAlaAsnValleuAspIleAspAspAspHe 1501 CTAAAGGAGGCTCCTCCAAATCCCTGGTGGCCAATGCTTCGACATGGACGACTTC	Oy 650 ArgHisAsnCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyr 669 1	Asn GCG Ile	749 PheThrMetPheAlaileLeuAlaThrileAlaValLeuLeuSerAlaProHisileile	Qy 769 Val 769 Db 1855 GTG 1857 RESULT 11 DME554209 LOCUS DME554209 1665 bp mRNA linear INV 01-APR-2003

us-09-303-232-2.rge

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Matches:
Conservative:
Mismatches:
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e 5	5/1 IntrodeCtroAlaThrSerAspAlaValProLeu
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qq	968 ITCAIGGICGICGGIGGIGGIGCIGACAGIAGIGGIGCICAACIACCACCAIGGACA 1027
δλ	ద.
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Db 1	088 ATCTTGCGAATGGGTCGACCCGGTCGCAAGATT
δλ	614 SerAspThrSerSerGluArgLysHisGlnIleLeuSerAspValGlu 629
Db 1	121ACACGCAAACAATACTATTAAGCAATCGCATGAAGGAGCTGGAG 1165
٥y	630 LeuLysGluArgSerSerLysSerLeuLeuAlaAsnValLeuAsplleAspAspAspPhe 649
1 qa	166 CIARAGGAGGGTCCTCCARATCCCTGCTGGCCAATGTCCTCGACATCGACGACGACGACTTC 1225
z Võ	650 ArgHisAsnCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyr 669
Db 1	226 CGGCACACAATA 1237
δy	670 ArgThrValTyrGlyGlnGlyAspAspGlySerIleGlyProIleGlySerThrArgMet 689
Db 1	238TCTGGCTCCCAAACGCCATTGGCTCGTCGGCCAGCTTCGGTCGG
ζ	690 ProAspAlaValThrHisHisThrCysIleLysSerSerThrGluTyrGluLeuGly 708
Db 1	283 CCACAACGGTGGAGGAGCATCACACGGCCATCGGCTG
λõ	709 LeulleLeulysGlulleArgPhelleThrAspGlnLeuArgLysAspAspGluCysAsn 728
Db 1	340 CTAATTCTCAAAGAATTGCAATTTATTACGGGGGGGGATGCGCAA
λŏ	729 AspIleAlaAsnAspIrpLysPheAlaAlaMetValValAspArgLeuCysLeuIleIle 748
Db 1	1400 GAATTGAICGGCGATTGGAAGTTCGCGGCAATGGTTGTGGTAGATTTTGTTAATTGTT
δλ	749 PheThrMetPheAlaileLeuAlaThrileAlaValLeuLeuSerAlaProHisileile 768
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δŏ	769 Val 769
Db 1	520 GTG 1522
RESULT 13 AF321447 LOCUS DEFINITION	2023 bp mRNA linear INV 29
ACCESSION	. (nACKAIpna-30D) mkNA, co
SOURCE	Drosophila melanogaster (fruit fly)

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ERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLMLSLEWNDYNLRWNETEYGGVK
DIRITPNKLWKPDVLMYNSADEGFDGTYHTNIVVKHSGSCLYVPPGIFKSTCKMDITW
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CCPEPYVDITFTIQIRRRILYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTIL
LSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFWVASSVVLTVVVLNYHRTADIHEM
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DFRHTISGSQTAIGSSASFGRPTVEEHHTAICCNHKDLHLIILKELQFITARWRKADD
EAELIGDWKPAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIVQ"
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GenBank Accession Number
                                                                   Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify
NNew and Highly Conserved Target of Adenosine Deaminase Acting on
Genetics 160 (4), 1519-1533 (2002)
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/note="results in asparagine to serine substitution;
compared to the sequence deposited in GenBank Accession
Number AE003626"
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 Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebbydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2023)
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Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford (
3QX, UK
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'product="nicotinic acetylcholine receptor
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/note="results in glycine
to the sequence deposited
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/db_xref="GI:20152849"
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/dev_stage="embryo"
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Naplahas, Dalphas and Dalphar, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
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 LeulysGluArgSerSerLysSerLeuLeuAlaAsnValLeuAspIleAspAspPhe
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/chromosome="2"
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1. .2110
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Grauso, M. and Sattelle, D.B.
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variant type V"
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/db_xref="G1:20152853"
/translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL
/note="ion channel; neurotransmitter transmembrane
receptor; alternatively spliced; contains exons 3a, 8a and
8b; contains two repeats of the transmembrane TM2 region"
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1678 ATTGGCTCGTCGGCCGGTCGGTCGGCCCACAACGGTC 700 LysSerSerThrGluTyrGluLeuGlyLeulleLeuLyS 1738GGCTGCAATCAAAGATCTTCTTCTTAATTCTTAAAT 720 GluLeuArgLysAspAspGluCysAsnAspIlealaAsi 1795 CGGATGCGCAAAGCTGACGACGAGCGGAATTGATGGG 740 VAlVAlAspArGCTGACGACGACGAGCGGAATTGATGGG 740 VALVALASpArGTTGTTTAATTGTTTTCAGGCTCTT 760 VAlLeuLeuSerAlaPrOHisIleIleVal 769 1915 GTGCTGCTCCCGCACAAAATCGT 769 1915 GTGCTGCTCCCGCACAATAATCGT 779		REFERENCE (Dases 1 to 3029) AUTHORS Schulet, T. Ociliade; Heliothinae;	Direct Submission Submitted (19-AFR-1999) ZF-BTB, Bayer 51368, Germany 1. 3029	/codon_start=1 /product="putative nicotinic acd 7-2 subunit" /protein_id="AAD32698.1" /fb xref="G1:4985007" /translation="WAPMLALALLEVVSI SEPLEVRFGLTLQQIIDVDEKNQLLITNIWLA KLWKEDVLWYNSAGGROGTYOTNVYNSAGG CDWKFGSWYYDGNQLDLVLKDEAGGDLSDFIT DVTFTIMIRRELLYFFNLIVPCVLISSMALI NIVAETLEPQVSDALFELISLTEAGTSSMALI NIVAETLEPQVSDALFELISTEAGTSSMALI GTSSMALINGTS	ent Scores: No.: t Similarity: ocal Similarity Match:
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                                      ------ddrcrchcadaadaa 169
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  Command line parameters:

MODEL=frame+_p2n.model -DEV=x1h

-Q=/Cogn2_1/USPTO spool/USG930323/runat_07052004_101109_23873/app_query.fasta_1.2261
-Q=/Cogn2_1/USPTO spool/USG9303232/runat_07052004_101109_23873/app_query.fasta_1.2261
-DB=N_Geneseq_29Jan04 -QFWT=fastap_-SUFFIX=rng_-MINMATCH=0.1_-LOOPE_1_0
-LOOPEXT=0_-UNITS_=bits_-START=1_-ENN=-1_-MATRIX=blosum62_-TRANS=human40.cdi
-LIST=45_-DCAALIGN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MIN=0_-ALIGN=15
-MODE_-LOCAL_-OUTFWT=pto_-NOFMEext_-HEAPSIZE=500_-MNILEN=0_-AXLIGN=25
-USER=USG9303232_@cGN_1_11200_@xrunat_07052004_110109_23873_-NCPU=6_-ICPU=3
-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG
-DEV_TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6
-FGAPEEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7_-
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Aaz24477 H. viresc
Abl27131 Drosophil
Abl27130 Drosophil
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Abl13733 Drosophil
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(without alignments)
4044.486 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                              nucleic search, using frame_plus_p2n model
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Delop 6.0 , Delext
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                                                                                                                                        This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere which neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies discussed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter condensor of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline
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                                                        New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.
                                                                                                                                                                                                                                                                                                                                              Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 U; 0 Other;
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on; plant protection agent; conductance; AChR; ds.
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotranamission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that aller conductance of ACHR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related ACHR in insects. (I) are also used to recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens
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                                                    nucleic acid encoding a nicotinic acetylcholine receptor octs, used to identify potential insecticides.
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This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens
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      nicotinic; insect; insecticide; screening; protection agent; conductance; AChR; ds.
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neurotransmission; plant
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P-PSDB; AAY50816.
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                              AspGluCysAsnAspIleAlaAsnAspTrpLysPheAlaAlaMetValValAspArgLew
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fo.: 8.57e-126 Length: 1498.50 Matches: Similarity: 98.69\$ Conservative: ocal Similarity: 97.38\$ Mismatches: fatch: 37.06\$ Indels:

984 297 4 1

-303-232-2 (1-770) x ABL27131 (1-984)

1 MetLysAsnalaGlnLeuLysLeuThrGluValAspAspAspGluLeuTrpLeuAlaVal 20

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371 MetAsnLeuArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProPro
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pharmaceutical; gene; ss.
                   Drosophila melanogaster.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176, ABL30511), expressed DNA sequences (ABL01840-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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TACGGCGCGGATGCGCAAAGCTGACGAAGCGGAATTGATCGGCGATTGGAAGTTCGC
                                                                            eThrAspGlnLeuArgLysAspAspGluCysAsnAspIleAlaAsnAspTrpLysPheAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 32863.
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ID NO 35681

developmental biology; cell signalling; insecticide;

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2000US-0191637P. 2000US-00614150.

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                             Drosophila melanogaster expressed polynucleotide SEQ
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                                                                                 pharmaceutical; gene; ss.
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11-JUL-2000;
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                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
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                               CGCCTATGGAAACCGGATGTACTGATGTACAACAGTGCCGACGAGGGCTTCGATGGAACG
                                               TyrGlnThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProProGly1le
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                                                                                                     MetLysPheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnLeuGlnAspGlu
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                                                                                                                                                                                                                                                                                                                                                                     biology; cell signalling; insecticide;
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                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                                                                              ProCysSerAspThrSerSerGluArgLysHisGlnIleLeuSerAspValGluLeuLys
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                                       ProTrp11eLeuArgMetSerArgProGlyArgProLeuIleLeuGluPheProThrThr
                                                                                                                                                                  AsnCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyrArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
ligand binding; ion channel; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuronal alpha-bungarotoxin binding protein alphal subunit cDNA.
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2 cDNA clones (AAM129196 and AAM59197) respectively code for the alphal subunit (AAM12368) and alpha2 subunit (AAM12365) of chick neuronal alphabungarctoxin binding protein (ABBP). They were isolated from an 18-day embryo chick brain cDNA library using a probe (see also AAT59198) based on the N-terminal amino acid sequence of chicken brain ABBP. The probe isolated partial clone pCh29-1, which encoded the N-terminal portion of alpha1. A subclone, pCh29-3 (ATC 40641), was used to rescreen the library, yielding clone pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence. A probe based on the C-terminal region of pCh31-1 was used obtain clone pCh34-1 (ATCC 40639), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further ABBP subunits, and in the recombinant prodn. of ABBP
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                                                                                                  New isolated neuronal alpha-bungaro-toxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 CTGATGCTGTGCTGCTGCGGCGCGCGCGCTGCGCGAGTCCCTGCAAGGAGAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2769 BP; 790 A; 604 C; 571 G; 804 T; 0 U; 0 Other;
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Neuronal alpha-bungarotoxin binding protein alpha 2; cholinergic; ligand binding; ion channel; ss. Neuronal alpha-bungarotoxin binding protein alpha2 subunit cDNA.

17-JUN-1997 (first entry)

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977 ATTGTTGGCCTCTCTGTTGTTGTCACTGTTATCGTTCTACAATACCATCACGATCCA 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGGGGGAAAAATGCCTAAATGGACAAGAGTCATCCTTCTGAATTGGTGCTTGGTTT 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAGGATGAAGAGACCAGGG-----GAAGATAAAGTGCGTCCCGCCTGT 1141
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                                919
                                                                                    GGGAAGAGAACTGAGAGCTTTTATGAGTGCTGTAAAGAACCATACCCAGATATCACATTC 736
                                                                                                                                  ACAGTAACCATGAGAAGGAAGGAAACTCTCTAACTAAGGGCTCAAACCTTCTTATTCCCTGTGTA 796
                                                                                                                                                                                             690 ProAspAlaValThrHisHisThrCysIleLysSerSerThrGluTyrGluLeuGlyLeu 709
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ThrGlyGlyAspIleSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValPro 491
                                                                                                                                                                            LeulleAlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeu 551
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                                                       GlylysArgAsnGlulleTyrTyrAsnCysCysProGluProTyrlleAspileThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrMetPheAlaIleLeuAlaThrIleAlaValLeuLeuSerAlaProHisIleIle 768
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                                                                                                                   AlailelleleArgArgArgThrLeuTyrTyrPhePheAsnLeullelleProCysVal
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2 CDNA clones (AAT59196 and AAT59197) respectively code for the alphal subunit (AAW12368) and alpha2 subunit (AAW12369) of chick neuronal alphabungarotoxin binding protein (ABBP). They were isolated from an 18-day embryo chick brain cDNA library using a probe (see also AAT59198) based on the N-terminal amino acid sequence of chicken brain ABBP. The probe alphal. A subclone, pCh29-1, which encoded the N-terminal portion of alphal. A subclone, pCh39-1 (ATCC 40641), was used to rescreen the library, yielding clone pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence. A probe based on the C-terminal region of pCh31-1 was used obtain clone pCh34-1 (ATCC 40639), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further ABBP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated neuronal alpha-bungaro-toxin-binding protein DNA - us screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 582 A; 406 C; 454 G; 659 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunits, and in the recombinant prodn.
                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 3A-B; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                          (SALK ) SALK INST BIOLOGICAL
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146. .1498
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56. .145
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                                                                                                                                                                                                                mat_peptide
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                                                                                                                                                                                     sig_peptide
                                                                                                              Gallus
                                                                                                                                          Key
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284

265 AsnSerSerSerSerSerSerSerAsnSerSerAsnAsnAsnSerSerThrGlnIleLeu

x AAT59197 (1-2101)

US-09-303-232-2 (1-770)

à a à

2101 244 85 129 109

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.36e-95 1170.50 58.02% 43.03% 28.95%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

61

295 121

--AsnGlyLeuAsnLysHisSerTrpIlePheLeu

285

standard; cDNA; 2101 BP

AAT59197 AAT59197

296 LeuIleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyrHisGluLysArgLeu 315

1157AGCTATCCCAACCCTCCAACCCTGAAAAACACAGAGATG	Oy 702 SerThrGluTyrGluLeuGlyLeuIleLeuLysGluIleArgPheIleThrAspGlnLeu 721	SULT 11 CS8395 AAC58395 AAC58395, 29-JAN-20 Human PRC Human; tru proliferer nootropic immunostin	KW hypothalamic disorder; glandular disorder; macrophagal disorder; KW inflammatory disorder; stromal disorder; blastocoelic disorder; KW inflammatory disorder; immunologic disorder; ss. KX XX FN W0200053755-A2. XX FN W62-DAN-2000, 2000W0-US000376. XX FN 08-MAR-1999; 99W0-US00528. FR 03-UN-1999; 99W6-0141037P. FR 23-UN-1999; 99W6-0141037P. FR 26-UUL-1999; 99WG-0145698P. FR 26-UUL-1999; 99WG-US0128313. FR 26-UUL-1999; 99WG-US028813. FR 26-UUL-1999; 99WG-US028813. FR 26-UUL-1999; 99WG-US028813.	(GETH) GENE Ashkenazi A
	396 ProAspValleuMetTyrAsnSerAlaAspGluGlyPheAspGlyThrTyrGlnThrAsn 396 ProAspValleuMetTyrAsnSerAlaAspGluGlyPheAspGlyThrTyrGlnThrAsn 407 CCTGALATTCTTCTTAACAGTGGGGATGAAGATTCGATGCAACTTTCAACAAAT 416 ValValValArgAsnAsnGlySerCysLeuTyrValProProGlyIlePheLysSerThr 417 (Db 587 iciriddacracagrachracacagarracaccracagacaracacracagae 637 476 IleserSerTyralLeuAsnGlyGluTrpGluLeuLeuGlyValProGlyLysArgAsn 495	S56 ThrileLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetProAlaThr 575	Db 1118 AAACCTGGGGAAAATATAAAGCCCTCTTGCAAATAT

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Wood WI;
    WPI; 2000-572270/53
     P-PSDB; AAB24088
Watanabe CK,
         Thirty PRO
            treatment,
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR0290, PR0341, PR0535, PR0619, PR07131, PR081039, PR081035, PR01103, PR01103, PR01103, PR01103, PR01181, PR01182, PR01182, PR01184, PR01187, PR01181, PR01182, PR01184, PR01187, PR01181, PR01281, PR01187, PR01181, PR01182, PR01184, PR01187, PR01181, PR02181, PR02182, PR01184, PR01187, PR01181, PR01182, PR01184, PR01187, PR01181, PR02181, PR02184, PR01187, PR01182, PR01184, PR01187, PR01181, PR01182, PR01184, PR01187, PR01184, PR0118 PRO polypeptides, useful in the of cancer. polynucleotides encoding diagnosis and prevention 50; Fig 57; 286pp; English Claim

G; 332 T; 0 U; 0 Other; Sequence 1509 BP; 297 A; 451 C; 429

cores: 8.22e-95 Length: 1509 1159.50 Matches: 237 dlarity: 60.76% Conservative: 82 Similarity: 45.14% Mismatches: 115 3 Gaps: 12	(-2 (1-770) x AAC58395 (1-1509)	IleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyrHisGluLys 313	ArgLeuLeuHi sAspLeuLeuAspProTyrAsnThrLeuGluArgProValLeuAsnGlu 333 :::	SerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGlnIlelleAspValAspGlu 353	LysasnglnleuleuValThrasnValTrpLeuLysLeuGluTrpAsnAspMetAsnLeu 373 	. ArgTrpasnThrSerAspTyrGlyGlyValLysAspLeuArg1leProProHisArg11e 393 :::	TrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspGlyThrTyrGln 413 	ThrasnvalvalvalargasnasnglysercysLeuTyrValProProGlyIlePheLys 433
Scores imilari I Simil ch:	-232-2	297 I 22 G	314 A : 82 A	334 S	354 L 202 A	374 A 262 C	394 T	414 T
Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match: DB:	US-09-303-232-2	Qy	Qy Db	Qy Db	Q _Y	Qy	oy Oy	oy Db

1227 973 GGCAAGATGCCCAAGTGGACCAGAGTCATCCTTCTGAACTGGTGCGCGTGGTTCCTGCGA 1032 ATGAAGAGGCCCGGGGGACAAGGTGCGCCCG---GCCTGCCAGCACAAGCAGCGGCGC 1089 -- ATCGGCTTCCGCGGCCTG 1176 473 493 672 732 553 792 573 852 581 581 723 743 913 GGCCTCTCGGTGGTGGTGACGGTGATCGTGCTGCAGTACCACCACCACGACCCCGACGGG 972 553 GCAGATATCAGTGGCTATATCCCCCAATGGAGAATGGGACCTAGTGGGAATCCCCCGGCAAG SerThrCysLysIleAspIleThrTrpPheProPheAspAspGlnArgCysGluMetLys PheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnLeuGlnAspGluThrGly 474 GlyAspIleSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValProGlyLys ArgAsnGlulleTyrTyrAsnCysCysProGluProTyrIleAspIleThrPheAlalle 514 IlelleArgArgThrLeuTyrTyrPhePheAsnLeuIlelleProCysValLeuIle AlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeu GlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetPro ------TrplleArglleValPheLeuCysTrpLeuProTrplleLeuArg ---ArgProLeuIleLeuGluPheProThrThrPro CysSerAspThrSerSerGluArgLysHisGlnIleLeuSerAspValGluLeuLysGlu -- Argadecercidecececece -----AsnCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPhe 669 TyrArgThrValTyrGlyGlnGlyAspAspGlySerIleGlyProIleGlySerThrArg ----TGTGGCCGC ---HisThrCysIleLysSerSerThr .228 ATGGCCTGCTCCCCCACGCACGATGAGCACCTCCTGCACGGTGGGCAACCCCCCGAGGGG GluTyrGluLeuGlyLeuIleLeuLysGluIleArgPheIleThrAspGlnLeuArgLys AspAspGluCysAsnAspIleAlaAsnAspTrpLysPheAlaAlaMetValValAspArg ArgSerSerLysSerLeuLeuAlaAsnValLeuAspIleAspAspPheArgHisrrrecercicercrraceaaccreercrrecarcrecacacacaca GCCAGCAACGGAACCTGCTGTAC----1177 GACGGCGTGCACTGTGTCCCG---ACCCCC AlaThrSerAspAlaValProLeu-TGCAGCCTGGCCAGTGTGGAG-MetProAspAlaValThrHis-MetSerArgProGly-442 502 613 673 534 574 853 597 1033 613 633 1204 689 434 454 494 554 793 582 1090 652 581

261

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393

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433 441 453 501 473

us-09-303-232-2.rng

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1033 ATGAAGAGGCCCGGGGAGGACAAGGTGCGCCGG---GCCTGCCAGCACAAGCAGCGGCGC 1089
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                                          LysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGluTrpAsnAspMetAsnLeu
                                                                                                    ArgTrpAsnThrSerAspTyrGlyGlyValLysAspLeuArgIleProProHisArgIle
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                1408 CTGTGCCTCATGGCCTTCTCGGTCTTCACCATCTGCACCATCGGCATCCTGATGTCG 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            social cell culture medium for treating cells and for inducing mammalian ll lines to conduct calcium ions, comprising specified concentrations ions of sodium, calcium and potassium at specified pH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the coding sequence for wild-type human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AABS0014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgleuLeuHisAspleuLeuAspProTyrAsnThrLeuGluArgProValLeuAsnGlu
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                                                                                                                                                                                                                            Wild-type human alpha7 ligand gated ion channel coding sequence
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                                                                                                                                                                                                                                                        Human; alpha7 nicotinic acetylcholine gated ion channel, 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Page 60-61; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MB;
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P-PSDB; AAB50012.
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                                                                                                                                                                     743
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rity of
                                                                                                                                     GACCCGGACTTGGCCAAGATCCTGGAGGGCCGCTACATTGCCAATCGCTTCCGCTGC
                                                                                                                                                                                                                                  LeuCysLeuIleIlePheThrMetPheAlaIleLeuAlaThrIleAlaValLeuLeuSer
                                                                                                                    GluTyrGluLeuGlyLeuIleLeuLysGluIleArgPheIleThrAspGlnLeuArgLys
                                                                                                                                                                    724 AspAspGluCysAsnAspIleAlaAsnAspTrpLysPheAlaAlaMetValValAspArg
                       TyrArgThrValTyrGlyGlnGlyAspAspGlySerIleGlyProIleGlySerThrArg
                                                                      -HisThrCysIleLysSerSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human neuronal nicotinic acetylcholine receptor subunits and DNA - al
transformed cells useful for screening cpds. which modulate activity
                                                                                                                                                                                                                                                                                                                                                                                                                Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA
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                                              GACTCTGGGGTAGTG
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GACGGCGTGCACTGTGTCCCG---ACCCCC-
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                         single receptor subunits or specific receptor subunit combinations with variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drug
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                                                                                                                                                                                                          identified e.g. screening with cells that express a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       574 TITGGGTCCTGGTCTTACGGAGGCTGGTCCTTGGATCTGCAGATGCAGGGG
                                                                                                                                                                                                                                                                       530 G; 423 T; 0 U; 1 Other;
in normal vs diseased brain tissues.
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                                                                                                                                                                                                                                                                                                 A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAW09025) of the human neuronal nicotinic acetylcholine receptor (TAChR). Host cells, est mammalian cells or amphibian oocytee, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT4832-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs
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GlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetPro
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                                                                                                                                                                     513
                                                                                                                                                                                             ACCATGCGCCGCAGGACGCTCTACTATGGCCTCAACCTGCTGATCCCCTGTGTGCTCATC 804
                                                                                                                                                                                                                                                                                                                                                                TCGCCCTCGCCCTGCTGCTTCCTGCAAAATTCCGGGAAAAATTCCCTG 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 ArgSerSerLevLevLevAlaAsnValLevAspIleAspAspAspPheArgHis--- 651
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PheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnLeuGlnAspGluThrGly 473
                                                                                                                                                                                                                                                                                                                                     534 AlaSerMetAlaLeuLeuGlyPheThrLeuProProAspSerGlyGluLysLeuSerLeu 553
                                                                                                                                                                                                                                                                                                                                                                                                                       GlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThrMetPro 573
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                                                                               GlyAspileSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValProGlyLys
                                                                                                       GCAGATATCAGTGGCTATATCCCCAATGGAGAATGGGACCTAGTGGGAATCCCCGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAsnGluIleTyrTyrAsnCysCysProGluProTyrIleAspIleThrPheAlaIle
                                                                                                                                                                                                                                                    514 IlelleArgArgArgThrLeuTyrTyrPhePheAsnLeuIleIleProCysValLeuIle
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|249 GACGGCGTGCACTGTGTCCCG---ACCCCC
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The invention relates to a method for identifying compounds that are antagonists or agonists of human neuronal nicotinic acetylcholine receptors (NAChRs), by contacting recombinant cells with a test compound and measuring ion flux, the electrophysiological response of the cells or binding of the test compound to the nNAChR. The recombinant cells are produced by transfection with a nucleic acid encoding at least one human NNAChR (alpha or beta) subunit, such that the cells express an nNAChR comprising one human subunit encoded by the transfected nucleic acid. This sequence represents cDNA encoding the alpha 7 subunit of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValCysLeuAlaGlyTyrHisGluLys 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to NNACHR.
                                                                                                                                                                                                                                                                                                Human neuronal nicotinic acetylcholine receptor alpha 7 subunit
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                                                                                                                                                                                                                                                                                                                                                     nNAChR;
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/product= "Human nNAChR alpha 7 subunit"
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73. .1581
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30-NOV-1992;
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Pred. No.:
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1359 1299 1479 1539 651 723 743 ------HisThrCysIleLysSerSerThr 703 1300 Ardeccrecrececcacededearcacerecrecaceseses 1480 CIGIGCCTCATGGCCTTCTCGGTCTTCACCATCATCTGCACCATCGGCATCCTGATGTCG 633 ArgSerSerLysSerLeuLeuAlaAsnValLeuAspIleAspAspRspPheArgHis----ATCGGCTTCCGCGGCCTG -----AsnCysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPhe 669 TyrArgThrValTyrGlyGlnGlyAspAspGlySerIleGlyProlleGlySerThrArg GluTyrGluLeuGlyLeuIleLeuLysGluIleArgPheIleThrAspGlnLeuArgLys 724 AspAspGluCysAsnAspIleAlaAsnAspTrpLysPheAlaAlaMetValValAspArg LeuCysLeuIleIlePheThrMetPheAlaIleLeuAlaThrIleAlaValLeuLeuSer -----GACTCTGGGGTAGT---1249 GACGGCGTGCACTGTGTCCCG---ACCCCCC---1207 GCCAGCAACGGGAACCTGCTGTAC---MetProAspAlaValThrHis-1540 dereceaacrregre 1554 764 AlaProHisIleIle 768 689 744 704 652

8, 2004, 19:29:44 completed: May {
1e : 850.783 secs Search con Job time :

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 11:31:03 ; Search time 18.738 Seconds (without alignments) 3952.801 Million cell updates/sec May Run on:

Title: Perfect score:

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELMLAV.....MFAILATIAVLLSAPHIIVS 770 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	nicotinic acetylch nicotinic acetylch nicotinic acetylch alpha-bungarotoxin nicotinic acetylch hypothetical prote hypothetical prote hypothetical prote nicotinic acetylch	
SUMMARIES		A24383
DB	04404040404040404040404040	7
Length	5002 5022 5022 5012 5012 5022 503 503 503 503 503 503 603 603 603 603 603 603 603 603 603 6	457
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acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetilch	nicotinic acetylch	acetylcholine rece	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	protein F25G6.4 [i	nicotinic acetylch	nicotinic acetylch	hypothetical prote	nicotinic acetylch	nicotinic acetylch	hypothetical prote
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ALIGNMENTS

REBULT 1 Abortance acetylcholine receptor alpha-7 chain precursor, neuronal - mouse nicotatic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse classes ans musculus (house mouse) C) Species and musculus (house mouse) C) Accession: A37175 ACCESSION: A37175 ACC
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Query Match 29.2%; Score 1179.5; DB 2; Length 502; Best Local Similarity 45.7%; Pred. No. 8.2e-77; Actober 237; Conservative 80; Mismatches 127; Indels 75; Gaps 9; Qy 295 LLIYLNLSAKVCLAGYHEKRILHDLLDPYNTLERPVLNESDPLOLSFGLTLMQIDDV 351 Db 6 LMLWILLAAGLVESERQKRIYKELLKNYNPLERPVANDSQPLTVYFTLSLMQINDV 65 Qy 352 DEKNQLLVTWWIKLEWNDMALKWNTSDYGGVKDLRIPPHRIWKPDVLMYNRADGCFDGT 411 Db 66 DEKNQLLTTNIWGLTTNIWGWNTSDYGGVKOVRFPDGLIMKPDILLYNSADERFDAT 125 Qy 412 YQTNVVVNRNGSCLYVPPGIFKSTCKIDTWFPPDDQRCEMKFGSWTYDGFQLDLGLQDE 471 CQY 412 YQTNVVVNRNGSCLYVPPGIFKSTCKIDTWFPPDDQRCEMKFGSWTYDGFQLDLGLQDE 471 CD 1	9y 472 TGGDISSYVINGEWELLGVPGKRNBIYYNCCPBPYIDITFAIIIRRRTLYYFFNLIIPCV 531 185ADISGYLSNGEWDLVGIPGKRTESFYECKCRPYPDITFTVTWRRTLYYGLNLLIPCV 242 9y 532 LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETWPATSDAVPL 581 1	PB 456 ichewfehasvvoricinarionimsherv 494 RESULT 3 T01378 T01378 T001378	
OY 582	RESULT 2 JUN0113 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken NiAlternate names: alpha-bungarotexin-binding protein alpha chain C;Species: Gallus gallus (chicken) C;Date: 12-Eeb-1993 #sequence revision 12-Feb-1993 #text_change 20-Aug-1999 C;Accession: JUN013; JH0172; S28018; B25738; S2656 R;Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.; Neuron 5, 847-856, 1990 A;Title: Neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentall A;Reference number: JN0113; MUID:91097796; PMID:1702646 A;Accession: JUN0113 A;Molecule type: DNA A;Residues: 1-502 <cou-> A;Coss-references: GB:K68586; NID:9287756; PIDN:CAA48576.1; PID:9287757 A;Experimental source: white leghorn; brain B;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron 5, 35-48, 1990 A;Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal subtypes of this A;Reference number: JH0172; MUID:90315188; PMID:2369519 A;Accession: JH0172, MUID:90315188; PMID:2369519 A;Accession: JH0172, MUID:90315188; PMID:2369519</cou->	A; Residues: 1-502 < CGC: A; Residues: 1-502 < CGC: A; Residues: 1-502 < CGC: A; Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078 A; Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078 A; Cross-references: D4A A; Reference number: S28018; MUID:93049204; PMID:1425587 A; Accession: S28018; MUID:93049204; PMID:1425587 A; Accession: S28018; MUID:93049204; PMID:1425587 A; Accession: S28018 A; Reference number: DAA A; Residues: 1-18 < CMAS A; Reference number: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320 A; Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320 A; Cross-references: EMBL:X68246; GB:S49751; NID:g65319; Dolly, J.O.; Lai, F.A.; Ray, N.; Ray, ContiTronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; Rayritle: Brain and muscle nicotinic acetylcholine receptors are different but homologous A; Reference number: A94055; MUID:85270494; PMID:3860855 A; Accession: B25738 A; Accession: B25738 A; Residues: 24-25.** EFF. 28-41, X., 43-45, X., 47 < CON> C; Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized	C;Genetics: C;Genetics: A;Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3 C;Superfamily: acetylcholine receptor C;Superfamily: acetylcholine receptor C;Superfamily: acetylcholine receptor C;Reywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein; F;1-23/Domain: signal sequence #status predicted <3G5- F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted <tr1- #status="" (asn)="" (covalent)="" (thr)="" (tyr)="" <tr2-="" <tr3-="" binding="" carbohydrate="" domain:="" f;26-280="" f;26-317="" f;415="" f;46,90,133="" phosphate="" predicted="" predicted<="" site:="" td="" transmembrane=""></tr1->

Db 187 DLQMLEADISNYISNGEWDLYGVPGKRNELYYECCKEPYPDVTYTITMRRRTLLYYGL 243 Qy			A/Gene: GDB:CHRNA7 A/Gene: GDB:CHRNA7 A/Gene: GDB:CHRNA7 A/Gene: GDB:CHRNA7 A/Gene: GDB:CHRNA7 A/Gene: GDB:CHRNA7 A/Gene: GDB:CHRNA7 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 A/Map position: 15q14-15q14 B/A/Onain: 15q14-15q14 B/A/Diading site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/B/Binding site: phosphate (Tyr) (covalent) #status predicted B/A/A/B/Binding site: phosphate (Tyr) (covalent) #status predicted
Db 128 TNVLVNASGHCQYLPPGIFKSSCYIDVRWFPFDVQQCKLKFGSWSYGGWSLDLQMQE 184 QY 474 GDISSYVLNGEWELLGVPGRNEIYYNCCPEPYIDITFAIIIRRRILYYFFNLIIPCVLI 533 185 ADISSYIPNGEWELLGVPGRNEIYYNCCPEPYIDITFAIIIRRRILYYFFNLIIPCVLI 244 QY 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNWVAETWPATSDAVPL	Qy 727 CNDIANDWKFAAMVVDELCLIFTMFAILATIAVLISAPHII 768 ::	A,Accession: JH0173 A,Molecule type: mRNA A,Residues: 1-511 <8CH> A,Kosicues: 1-511 <8CH> A,Kosicues: 1-511 <8CH> A,Kross-references: GB:X52296; NID:g63081; PIDN:CAA36544.1; PID:g63082 A,Experimental source: brain A,Mote: this sequence is similar to acetylcholine receptor alpha chains C,Comment: Alpha-bungarotcoxin binding proteins are localized to extrasynaptic pseudodend C,Superfamily: acetylcholine receptor C,Keywords: glycoprotein; transmembrane protein F;1-30/Domain: signal sequence #status predicted <sig> F;31-510/Product: alpha-bungarotcoxin binding protein alpha-2 chain #status predicted <ab #status="" <tml="" domain:="" f;239-262="" predicted="" transmembrane=""> F;230-280/Domain: transmembrane #status predicted <tml> F;304-333/Domain: transmembrane #status predicted <tml> F;304-200main: transmembrane #status predicted <tml> F;304-300main: transmembrane #status predicted <tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></tml></ab></sig>	F;479-496/Domain: transmembrane #status predicted <tw4. #status="" (asn)="" (covalent)="" 100;="" 117;="" 12;="" 238;="" 285="" 344="" 44.2%;="" 5.6e-76;="" 83;="" :="" best="" binding="" carbohydrate="" conservative="" f;54="" gaps="" indels="" local="" match="" matches="" mismatches="" nginkhsmiflitylnisakvclagyhekrlihdldpyntlerpvinesdplqlsfglt="" no.="" pred.="" predicted="" query="" qy="" similarity="" site:="" td="" ="" <=""></tw4.>

Db 185 ADISGYIPNGEWDLYGIPGKRSERPYECCKEPYPDVTFTVTWRRTLYYGLNLLIPCVLI 244 QY 534 ASWALLGFTLPPDSGEKLSLGYTILLSLTVFLNWVAETMPATSDAVPL	OY 669 YRTUYGGGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDDLRK 723 : : : :	RESULT 7 S6588 Siocinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis CiSpecies: Caenorhabditis elegans C;Species: Gener-1996 Hasquence_revision 07-Feb-1997 #text_change 20-Aug-1999 C;Accession: S68588; S57496 C;Accession: S68588; S57496 C;Accession: S68588; S57496 A;Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans. A;Reference number: S68587; MUID:96196478; PMID:8627624 A;Accession: S68588 A;Access	C; Superfamily: acetylcholine receptor C; Superfamily: acetylcholine receptor C; Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane, r. 1-19/Domain: signal sequence #status predicted <sig. #status="" 1104;="" 139;="" 2.1e-71;="" 20-498="" 227;="" 27.3*;="" 295="" 2;="" 354="" 43.3*;="" 498;="" 76;="" 82;="" 8;="" <mat.="" acetylcholine="" alpha-1="" best="" chain="" conservative="" db="" f;="" gaps="" indels="" length="" lliyinisakvclagyhekrlhdlldpyntlerpvlnesdplqlsfgltlmqiidvdek="" local="" match="" matches="" mismatches="" nicotinic="" no.="" pred.="" predicted="" product:="" query="" qy="" receptor="" score="" similarity="" th="" ="" <=""><th>OY 415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474 :: : : : </th><th>OY 534 ASMALIGETLPPDSGEKLSLGVTILLSLTVFLNWYAETWPATSDAVPL 581 Db 244 TLMTLLGFTLPPDAGEKTTLOITVLLSICFPLSIVSEMSPPTSEAVPLLGIFFTCCMIVV 303 Qy 582</th></sig.>	OY 415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474 :: : : :	OY 534 ASMALIGETLPPDSGEKLSLGVTILLSLTVFLNWYAETWPATSDAVPL 581 Db 244 TLMTLLGFTLPPDAGEKTTLOITVLLSICFPLSIVSEMSPPTSEAVPLLGIFFTCCMIVV 303 Qy 582
Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12; Qy 1:	QY 474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFRLIIPCVLI 533 Db 185 ADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVTFTVTMRRTLYYGINLLIPCVLI 244 QY 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVPLNWVAETMPATSDAVPL 581 Db 245 SALALLVFLLPADSGEKLSLGTVLLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304	QY 582	RESULT 6 G02259 alpha 7 neuronal nicotinic acetylcholine receptor - human C,Species: Homo sapiens (man) C,Species: Homo sapiens (man) C,Grecesion: G02259 R;Leonard, S. submitted to the EMBL Data Library, November 1995 R;Accession: G02259 A;Accession: G02259 A;Accession: G02259 A;Accession: G02259 A;Accession: Logo: MRMA A;Reference number: H00336 A;Accession: G02259 A;Crossion: L-SO2-C-LEO A;Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077 C;Superfamily: acetylcholine receptor	Query Match 28.6%; Score 1155.5; DB 2; Length 502; Best Local Similarity 45.1%; Pred. No. 4.3e-75; Pred. Similarity 45.1%; As.1%; Pred. No. 4.3e-75; Matches 237; Conservative 80; Mismatches 117; Indels 91; Gaps 12; Qy 297 IYLNLSAKVCLAGYHEKRILHDILIDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353 :: :	QY 354 KNOLLVTNVWLKLEMNDMNLRWNTSDYGGYKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413

RESULT 9 T19622 hypothetical protein C31H5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 C;Accession: T19622 R;Kershaw, J. submitted to the EMBL Data Library, April 1997 A;Reference number: 219153 A;Accession: T19622	iminary; translated from GB/EMBL/DDBJ et DNB et DNB nces: EMBL: Z93778; PIDN: CAB07843.1; GSI gource: clone C31H5 31H5.3 11; 70/3; 139/2; 270/1; 299/1; 336/3; 37 acety1choline receptor	Dest Local Similarity 37.2%; Pred. No. 5.2e-63; Dength 350; Matches 214; Conservative 85; Mismatches 152; Indels 124; Gaps 1 Qy 293 IFLLIYLNLSARVCLACYHEKELLHDLIDPYNTLERPVLNESDPLQLSFGLTLMOIIDVD 35	413 OTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDDEIL 132 PUNAVULYTGNVTWIPPAIIRSSCAIDIAYFPFDTQHCTMKFGSWTYSGFFTDLINT 473 GGDISSYVLNGEWELLGYPGKRNBIYYNCCPEPYIDITFAIIIRRRILYYFFNLLIPCVL		614 614 365 639 639	675 GGDDGSIGPIGGTRMPDAVTHHTCIKSSTEYELGLILKEIRPITDQLRKDDECNDIANDW 1.	RESULT 10 T19862 hypothetical protein C40C9.2 - Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: L5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C,Accession: T19862
Db 362 TKPNRH	RESULT 8 T25671 hypothetical protein D2092.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15.0ct-1999 #sequence_revision 15-0ct-1999 #text_change 21-Jan-2000 C;Accession: T25671 R;Gattung, S.; Maggi, L. R;Gattung, S.; Maggi, L. A;Gattung, S.; Maggi, L. A;Beference number: Z20067 A;Reference number: Z20067 A;Reference number: Z20067 A;Status: Dreliminary: translated from GR/RMRI/DDRJ A;Status: Dreliminary: translated from GR/RMRI/DDRJ	A; Molecule type: DNA	Ouery Match 25.0%; Score 1009.5; DB 2; Length 461; Best Local Similarity 39.4%; Pred. No. 1.1e-64; Matches 209; Conservative 80; Mismatches 126; Indels 115; Gaps 10; Qy 283 ILNGLNKHSWIFLLIYLNLSARVCLAGYHERRLHDLLDPYNTLERPVLNESDPLQLSFG 342	243 LTLMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLM 400		QY 577 DAVPLWIRIVELCWLPWILRMSR 599 1	

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rshaw, J.
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trons: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
perfamily: acetylcholine receptor
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thetical protein C31H5.3 - Caenorhabditis elegans
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cession: T19622
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Aigene: Flybase: Lacepaa
Aintrons: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
Aintrons: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
Aintrons: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
Aintrons: 64/3; 79/3; 116/2; 176/3; 116/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 176/2; 1
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nicotinic acetylcholine receptor alpha-Ll chain precursor - desert locust
cispecies: Schistocerca gregaria (desert locust)
cispecies: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
Ciscession: S12259
EMBC 48:Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Das EMBO J. 9, 4391-4398, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 KQTADSDNIEVGIDLQDYYISVEWDIMRVPAVRNEKFYSCCEEPYLDIVFNLTLRRKKTLF
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Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576 Note: 538-Tyr was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Mismatches 168; Indels 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 889; DB 1;
Pred. No. 6.6e-56;
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521 IACVVGTALIILQAPSL 537
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35.2%;
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Best Local Similarity 35.24
Matches 196; Conservative
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A.Accession: S00381, MUD:9755; PIDN:CAA30172.1; PID:97576
A.Accession: Ballivet, M.; Spierer, P.
BMBO J. 7, 611-618, 1988
A.Accession: S00381, MUD:828626; PMD:2840281
A.Accession: S00381, MUD:8285626; PMD:2840281
A.Accession: S00381, MUD:8285626; PMD:2840281
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   R;Hembry, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Accession: T19862
A;Accession: T19862
A;Accession: T19862
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-542 <MIL>
A;Residues: 1-542 <MIL>
A;Cross-references: EMBL: Z70266; PIDN: CAA94206.1; GSPDB: GN00028; CESP: C40C9.2
A;Experimental source: clone C40C9
C;Genetics:
A;Genetics:
A;Genetics:
A;Map position: X
A;Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; C;Superfamily: acetylcholine receptor
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nicotinic acetylcholine receptor alpha-2 chain precursor - fruit fly (Drosophila melanog C; Species: Drosophila melanogaster C; Species: Drosophila melanogaster C; Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 21-Jun-2002 C; Accession: S11679; S10306; $11084 R; Sawruk, E.; Schloss, P.; Betz, H.; Schmitt, B. BMBO J. 9, 2671-2677, 1990 A; Title: Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel dev A; Reference number: S11679; MUID:90360975; PMID:1697262 A; Accession: S11679.
submitted to the EMBL Data Library, June 1990
A; Description: Nucleotide sequence of the mature human nicotinic acetylcholine receptor A; Reference number: $21338
A; Accession: $21338
A; Accession: $21338
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 30-503 <ANA
A; Residues: 30-503 <ANA
A; Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C; Genetics: A; Cross-references: GDB:125219; OMIM:118503
A; Cross-references: GDB:125219; OMIM:118503
A; Map position: 15g24-15g24
C; Superfamily: acetylcholine receptor
C; Keywords: neurotransmitter receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 NQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
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A;Residues: 1-576 <SAW>
A;Residues: 1-576 <SAW>
A;Cross-references: EMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533
A;Note: 232-Ile was also found
B;Baumann, A.; Jonas, P.; Gundelfinger, E.D.
Nucleic Acids Res. 18, 3640, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 503;
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
20.9%; Score 845; DB 2;
Best Local Similarity 35.2%; Pred. No. 8.1e-53;
Matches 178; Conservative 97; Mismatches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             762
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                                                                                              A; Residues: 1-557 mans.

A; Residues: 1-557 mans.

A; Residues: 1-557 mans.

A; Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134

A; Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134

C; Superfamily: acetylcholine receptor
C; Reywords: glycoprotein; on channel; neurotransmitter receptor; transmembrane protein
C; Reywords: glycoprotein; on channel; neceptor alpha-L1 chain #status predicted <NIS-
F; 24-557, Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAI
F; 245-266, Domain: transmembrane #status predicted <TM1>
F; 200-229, Domain: transmembrane #status predicted <TM3>
F; 308-329, Domain: transmembrane #status predicted <TM3>
F; 308-329, Domain: transmembrane #status predicted <TM4>
F; 3108-329, Domain: transmembrane #status predicted <TM4>
F; 3108-329, Domain: transmembrane #status predicted <TM4>
        nicot
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A,Title: Sequence and functional expression of a single alpha subunit of an insect A,Reference number: S12359; MUID:91092263; PMID:1702381
A,Accession: S12359
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ಹ
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTY 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDL----QL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 MTKAVLHHTGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWTYDGDQIDLKHINQK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDE----TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFF 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: | : | : ||:||:||:| XDDNKVKVGIDLREYYESYVEWDILGVPAERHEKYYPCCAEPYPDIFFNITLRAKTLEYTV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --CRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475
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C.Species: Home sapiens (man)
C.Date: 07-Oct-1994 #text_change 20-Aug-1999
C.Accession: A53956; 821338
R.Mihovilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1918
A.Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of A.Reference number: A53956; MUID:91114756; PMID:1989896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIRIVFLCWLPWILRMSRPGRPLILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 YLLFTMVLVGLSVVITIMVLNVHYRKPSTHKMAPWVRKVFIRRLPKLLLMRVPEQLL---
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A;Cross-references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
R;Anand, R.; Lindstrom, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 2; I
9.1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                               21.6%; Score 873; 36.8%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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A;Status: prelimina:
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A; Status: mucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 42-90, 1', 92-576 <JON>
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A;Title: Sequence of D-alpha-2, a novel alpha-like subunit of Drosophila nicotinic acety
A;Reference number: S10306; MUID:90301489; PMID:2114015
A;Accession: S10306
                                                                                                                                                                    A;Cross-references: EMBL:X52274; NID:97802; PIDN:CAA36517.1; PID:97803
R;Jonas, P.; Baumann, A.; Merz, B.; Gundelfinger, B.D.
FEBS Lett. 269, 264-268, 1990
A;Title: Structure and developmental expression of the D-alpha-2 gene encoding a novel A;Reference number: S11084; MUID:90353591; PMID:2117557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 HSW----IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404
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Best Local Similarity 34.48
Matches 193; Conservative
                                                                                                       A; Molecule type: mRNA
A; Residues: 1-576 <BAU>
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nicornic acetylcholine receptor nonalpha chain precursor - fruit fly (Drosophila melano (Species: Drosophila melanogaster C; Species: Drosophila melanogaster C; Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 22-Jun-1999 C; Accession: 803012; A38064; Ā26313; A28126; A38759 R; Sawruk, E.; Hermans-Borgmeyer, I.; Betz, H.; Gundelfinger, B.D. FEBS Lett. 235, 40-46, 1988 Gran invertebrate nicotinic acetylcholine receptor gene: the A; Reference number: S03012; MUID:88296842; PMID:3136037
                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-72, VV, 74-521 cHER>
A,Gross-references: BMBL:X04016; NID:97537; PIDN:CAA27641.1; PID:97538
R,Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
R,Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
R,Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
A,Title: Expression of a Drosophila melanogaster acetylcholine receptor-related gene in
A,Reference number: A28126; MUID:88174720; PMID:2832736
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A;Introns: 22/1; 67/3; 119/2; 267/3; 467/3
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane
F;1-24/Domain: signal sequence #status predicted <8IG>
F;25-521/Product: nicotinic acetylcholine receptor nonalpha chain #status predicted <MA*
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Fig5-26/Domain: transmembrane #status predicted <TM1>
Fig6-285/Domain: transmembrane #status predicted <TM2>
Fig0-333/Domain: transmembrane #status predicted <TM2>
Fig2-333/Domain: intracellular #status predicted <TM3>
Fig2-34481/Domain: intracellular #status predicted <TM3>
Fig8-250/Domain: transmembrane #status predicted <TM4>
Fig8-150/Domain: transmembrane #status predicted <TM4>
Fig8-150/Domain: stansmembrane #status predicted <TM4>
Fig8-152-166/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: ard
A;Cross-references: FlyBase:FBgn0000038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-521 <WAD>
A,Cross-references: EMBL:M20316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A28126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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187 NKNFVDLSDYWKSGTWDIIEVPAYLN-VYEGDSNHPTETDITFYIIIRRKTLFYTVNLIL 245	529 PCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNNVAETMPATS 576	246 PTVLISFLCVLVFYLPAEAGEKVTLGISILLSLVVFLLLNSKILPPTSLVLPLIAKYLLLF 305	Q	306 TFIMNTVSILVTVIIINWNFRGPRTHRMPMYIRSIFLHYLPAFLFMKRPRKTRLRMMMEM 365	SSKSLL) 366 PGMSMPAHPHPSYGSPAELPKHISAIGGKQSKMEVMELSDLHHPNCKINRKVNSGGEL 423	THHTCIKSSTEYELGLILK		DECNDIAN	463 DLYIQTREDWKYVAMVIDRLQLYIFFIVTTAGTVGILMDAPHI 505
187	529	246	577	306	612	366	665	424	725	463
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Search completed: May 7, 2004, 11:39:30 Job time : 20.738 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

7, 2004, 11:18:28 ; Search time 14.3803 Seconds (without alignments) 2788.120 Million cell updates/sec May Run on:

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

141681 Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

*	Description		2770 gall	1 rattus	544 homo sa	_	_	_		schisto		homo	droso	P04755 drosophila	qallus	gallus	31 gallus	9 rattus	7 rattus	bos tau	P18845 carassius	drose		gallı		homo	756 mus m	~	143 rattus	963	5108 r	53 dallus	184 gallus	74 mus mus
SUMMARIES	JD	ACH7 MOUSE	ACH7 CHICK	ACH7 RAT	ACH7 HUMAN	ACH7_BOVIN	ACH1 CAEEL	ACH1_DROME	ACH1 MANSE	ACH1 SCHGR			ACH2 DROME	ACH3_DROME	ACH2_CHICK		ACH3 CHICK	ACH2 RAT		ACH3 BOVIN	ACH3_CARAU	ACH4_DROME	ACHP HUMAN	ACH6_CHICK	ACHA_BOVIN	ACH6_HUMAN	ACHA_MOUSE	ACH2 XENLA	ACH6 RAT	ACH8 CAEEL	ACHA_RAT	ACHP_CHICK	ACHN CHICK	ACH4_MOUSE
	Length DB	502 1				499 1										456 1	496 1				512 1								93		457 1	470 1	_	29
مين	Query Match Length	29.2	29.5	29.0	28.7	28.6	27.3	22.0	21.9	21.6	21.0	20.9	20.9	20.8	20.7	20.5	20.5	20.5	20.4	20.3	20.3	20.5	19.9	19.9	19.8	19.8	19.7	19.7	19.6	19.6	19.5	19.5	19.5	19.5
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098880 brachydanio	P02711 torpedo mar	P12392 rattus norv	P12390 rattus norv	P17787 homo sapien	P02708 homo sapien	P43681 homo sapien	P09482 gallus gall	P02710 torpedo cal	P22456 xenopus lae	P12391 rattus norv	P19370 carassius a
ACHA BRARE	ACHA_TORMA	ACHP_RAT	ACHN_RAT	ACHN_HUMAN	ACHA HUMAN	ACH4 HUMAN	ACH4 CHICK	ACHA_TORCA	ACH1 XENLA	ACHO_RAT	ACHN_CARAU
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456	461	495	200	502	482	627	622	461	457	464	459
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19											
		783	782.5	782	780	780	779.5	779	773.5	772	769.5

ALIGNMENTS

EXTRACELLULAR (POTENTIAL).

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23

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                                                                                                                                                                                            297 IYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353
                                                                                                                                                                                                                                          354 KNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
                                                                                                                                                                                                                                                                                        414 INVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETG 473
                                                                                                                                                                                                           TNVLVNASGHCQYLPPGIFKSSCYIDVRWFPFDVQQCKLKFGSWSYGGWSLDLQMQE---
                                                                                                                                                                                                                                                                                                                                                  -----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
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                                                                                                                                                                                                                                                                                                                                      GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 GLSVVVTVIVLRYHHHDPDGGKMPKWTRIILLINWCAWFLRMKRPGEDKVRPACQHKPRR-
                                                                                                                                                                       Gaps
        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                   (LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
C9312E5226D120E3 CRC64;
                                                                                                                                                                       85;
                                                                                                                                               29.2%; Score 1182.5; DB 1; Length 502; 45.8%; Pred. No. 5.1e-75; ive 80; Mismatches 118; Indels 85;
                                                                                                                                                                                                                                                                                                                                                                                 534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 CNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEVICSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
                                                                              (BY SIMILARITY)
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CARBOHYD
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                                                                                                                            SEQUENCE
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Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                         MEDLINE=91097796; PubMed=1702646; Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S., Millar N., Valera S., Barkas T., Ballivet M.;
                                                                                              Neuronal acetylcholine receptor protein, alpha-7 chain precursor
                                        72.2.7.7
1-20G-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
               502 AA
               STANDARD;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                  TISSUE=Brain;
             ACH7_CHICK
P22770;
                                                                                                                                                                Gallus
ACH7_CHICK
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"Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor promoter develops during morphogenesis of the central nervous uronal nicotinic acetylcholine receptor subunit (alpha 7) is opmentally regulated and forms a homo-oligomeric channel blocked Ray N., Raftery M.A.; "Brain and muscle nicotinic acetylcholine receptors are different but Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A., MEDLINE-92049732; PubMed-1719423; Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C., Hussy N., Bertrand S., Ballivet M., Changeux J.-P.; "Mutations in the channel domain alter desensitization of a neuronal MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
MEDLINE=93024917; PubMed=1383829;
Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
Changeux J.-P., Bertrand D.;
"Mutations in the channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic.";
Nature 359:500-505(1922).

-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J.; Brain alpha-bungarctoxin binding protein cDNAs and Mabs reveal subtypes of this branch of the ligand-gated ion channel gene superfamily."; Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M., Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985). SEQUENCE OF 1-18 FROM N.A. STRAIN=White leghorn; TISSUE=Erythrocyte; TISSUE=Brain; MEDLINE=85270494; PubMed=3860855; MEDLINE=90315158; PubMed=2369519; MEDLINE=93049204; PubMed=1425587 EMBO J. 11:4529-4538(1992) nicotinic receptor."; Nature 353:846-849(1991). MUTAGENESIS OF LEU-270. Neuron 5:847-856 (1990) Neuron 5:35-48(1990). proteins. SEQUENCE OF 24-47. SEQUENCE FROM N.A. alpha-BTX Matter J.M.; neuronal homologous system. HERE BERKER BERKER

membrane.

SUBUNIT: Forms a homo-oligomeric channel blocked by alphabungarotoxin. The structure is probably pentameric (By

This SWISS-PROT entry is copyright. It is produced through a collaboration similarity).
SUBCELUGAR LOCATION: Integral membrane protein.
DEVELOPMENTAL STAGE: Alpha-7 transcripts transiently accumulate in the developing optic tectum between E5 and E16.
SIMILARITY: Belongs to the ligand-gated ionic channel family.

between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):

EMBL; X52295; CAA36543.1; ... EMBL; X68246; CAA48317.1; ... EMBL; X68586; CAA48576.1; -.. PDB; 1KC4; 17-APR-02. PIR; JN0113; JN0113.

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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     670 RTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECND 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----CGRMICSPTEEENLLHSGHPSEGDPDLAKILEEVRYIANRFRDQDEEEA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 LLIYLNLSA---KVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEKNOLL VINVMLKLEMNDMNLRMNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 TGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRILYYFFNLIPCV
                                                                                                                                                               NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 QHKQRRCS--LSSMEMNIVSGQQCSNGNMLYI--GFRGLDGVHCTPTIDSGVI----
                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
L->S, T: SUPPRESSES INHIBITION BY THE OPEN-CHANNEL BLOCKER QX-222.
QR -> ET (IN REF. 3).
S72325D4309AD2FD CRC64;
                                                                                                                                                                                                                                                                                ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                         75;
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 502;
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PDB; 1KL8; 17-APR-02.
InterPro; IRR006029; Neu channel memb.
InterPro; IRR006202; Neur chan LBD.
InterPro; IRR006201; Neur chan LBD.
Pfam; PF02911; Neur chan LBD; 1.
Pfam; PF02912; Neur chan LBD; 1.
PRINTS; PR00252; NEUR-Chan LBD; 1.
PRINTS; PR00252; NEUR-DANNEL.
IIGREMAS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROIR LON CHANNEL; 1.
PROSITE; PS00236; NEUROIR LON CHANNEL; 1.
PROSITE; PS00236; NEUROIR LON CHANNEL; 1.
PROSITE; PS00236; NEUROIR LON CHANNEL; 1.
PROSITE; PS00236; NEUROIR LON CHANNEL; 1.
PROSITE; PS00236; NEUROIR LON CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        127; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            29.2%; Score 1179.5; DB 1
45.7%; Pred. No. 8.2e-75;
tive 80; Mismatches 127;
                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                           ALPHA-7 CHAIN
EXTRACELLULAR
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56946 MW;
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RESULT 3

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Muxinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BÝ SIMILARITY.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93147931; PubMed=7678857; Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.; "Molecular cloning, functional properties, and distribution of rat brain alpha 7: a nicotinic cation channel highly permeable to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1998) to the EMBL/GenBank/DDBU databases.
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                          01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
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(By
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PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms a homo-oligomeric channel blocked by bungarotoxin. The structure is probably pentameric (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
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  502 AA.
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PIR; T01378; T01378.
InterPro; IPR006020; Neuc channel memt
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur chan LBD.
Ffam; PF02931; Neur chan LBD; 1.
PRANTS; PR00293; Neur chan LBD; 1.
PRANTS; PR00282; NETCONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley; TISSUE=Brain;
  PRT;
                    Q05941;
01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurosci. 13:596-604(1993)
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  STANDARD;
                                                                                                                                                                                              Rattus norvegicus (Rat).
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213
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                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                   CHRNA7 OR ACRA7.
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TISSUE-Hippocampus;
SEQUENCE FROM N.A.
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Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
"Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SYSY cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus occytes.";
Mol. Pharmacol. 45:546-554(1994).
                                                                                                                                                                                                                                                    CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTV
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                                                                                                                                                                                                                                                                                 534 ASMALLGFTLPPDSGEKLSLGVTIILSLTVFLNMVAETMPATSDAVPL------
                                                                                                  Gaps
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACH7_HUMAN STANDARD; PRT; 502 AA.
P36544; Q15826; Q96RH2; Q99555; Q9BXH0;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N -> F (IN REF. 2).
P -> R (IN REF. 2).
                                                                                                  85;
                                                                              DB 1; Length 502;
                                                                             29.0%; Score 1173.5; DB 1; Length
45.6%; Pred. No. 2.1e-74;
.ive 80; Mismatches 119; Indels
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                                                           00996E74EC7B9A56 CRC64;
  SIMILARITY)
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  BY
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Mammalia; Eutheria; Primates;
                                                            56410 MW;
                                                                                                   Conservative
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90
133
447
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133
447
469
502 AA;
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                                                                                         Similarity
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                                                                                                  Matches 238;
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                   CARBOHYD
                                       CONFLICT
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           CARBOHYD
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MEDLINE=97162233; PubMed=9009220; Groot Kormelink P.J., Luyten W.H.M.L.; Groot Kormelink P.J., Luyten W.H.M.L.; Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and chromosomal localization of the human alpha 'nicotinic receptor subunit gene (CHRNA7).";
Genomics 19:379-381(1994).
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                                                                                                           SEQUENCE FROM N.A.

MEDILINE=97062879; PubMed=8906617;

Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,

Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;

"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herath A.,
Page M.J.,
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Chini B., Raimondi B., Elgoyhen A.B., Moralli D., Balzaretti M.,
Heinemann S.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cluster analysis of an extensive human breast cancer cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Forms a homo-oligomeric channel blocked by alphabungarotoxin. The structure is probably pentameric (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M. Lee J., Tian J., Giordano T.;
"Cloning and sequence of the human a7 nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUB=Epidermal keratinocytes;
Arredondo J., Grando S.A.;
"Cloning cholinergic receptors in human keratinocytes.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Groot Kormelink P.J., Luyten W.H.M.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-21829512; PubMed=11840567;
Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L.,
Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A.,
Zvelebil M.J.;
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Proteomics 2:212-223(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Neurosci. 7:217-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drug Dev. Res. 30:252-256(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 line SH-SY5Y and/or IMR-32."
FEBS Lett. 400:309-314(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 24-502 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 17-502 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Retina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor
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-----DSGVV----CGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRC 449
                                                          245 SALALLVFLLPADSGEKISLGITVLLSLTVFMLLVABIMPATSDSVPLIAQYFASTMIIV 304
                                                                                                                                                                                                                                                                                              305 GLSVVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCAWFLRMKRPGEDKVRP-ACQHKQRR 363
                                                                                                                                                                                                                                                                                                                                                 CSDTSSERKHQILSDVELKERSSKSLLANVLDIDDDFRH----NCRPMTPGGTLPHNPAF 668
68 KNQVLTINIWLQMSWIDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDATFH 127
                                                                                                                                                                                                                                                                                                                                                                                                                            669 YRTVYGQGDDGSIGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFITDQLRK 723
                                                                                                                                     185 ADISGYIPNGEMDLVGIPGKRSERFYECCKEPYPDVTFTVTWRRRTLYYGLNLLIPCVLL
                                                                                                               474 GDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLI
                                                                                                                                                                                                                                                                      -----WIRIVFLCWLPWILRMSRPG----RPLILEFPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both long and short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromaffin cells: molecular cloning, functional expression and alternative splicing of the alpha 7 subunit.";

Bur. J. Neurosci. 7:647-655(1955).

-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cr-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=P54131-2; Sequence=VSP 000075; Isold=P54131-2; Sequence=VSP one chromaffin cells. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-bugarctoxin. The structure is probably pentameric (by similarity). Homo-oligomer of the short form gives rise to unfunctional channels, as does coexpression of both long an
                                                                                                                                                                                           534 ASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL---
                                                                                                                                                                                                                                                                                                                                                                                       364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCVP-TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 QDESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSADNFV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         724 DDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P54131-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forms of the receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
NCBL TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Long;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOVIN
                                                                          128
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                                                                                                                                                                                                                                                                                                                                                 613
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BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 IYLNLSAK---VCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 KNQLLVTNVWLKLEWNDMNLRMNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSALL,
Transmembrane, Louis BY SIMILARITY.
SIGNAL 1 22 BY SIMILARITY.
SIGNAL 23 502 NECRONAL ACETYLCHOLINE RECEPTOR PROTEIN,
ALPHA-7 CHAIN.
ALPHA-7 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULÂR LOCATION: Integral membrane protein.
MASS SPECTROMETRY: MW-54157.68; METHOD=MALDI.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. GO; GO:0015464; F:acetylcholine receptor activity; TAS. GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. GO; GO:0000187; P:acetivation of MAPK; TAS. GO:0006810; P:transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A -> G (IN REF. 1 AND 7).
S -> N (IN REF. 2 AND 6).
S -> P (IN REF. 2 AND 6).
C -> S (IN REF. 8).
A -> G (IN REF. 1).
RMACS -> AWPAP (IN REF. 8).
W; D94B3A482EAA0E42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 2e-73;
82; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.7%; Score 1159.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006029; Neu channel memb.
InterPro; IPR006202; Neur channel memb.
InterPro; IPR006201; Neur channel.
Pfam; PF02931; Neur chan IBD; 1.
Pfam; PF02032; Neur chan memb; 1.
PRINTS; PR0252; NRIONCHANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                              EMBL; U62436; AAB40114.1; -...
EMBL; Y08420; CAA6697.1; -...
EMBL; L25827; -; NOT ANNOTATED CDS.
ENBL; Z23141; CAA80672.1; -...
EMBL; AP32758; AAKI9515.1; -...
EMBL; AP32758; AAKI9515.1; -...
PIR; G02259; G02259.
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                                                                                                                                                                                                                                        EMBL; X70297; CAA49778.1; -. EMBL; U40583; AAA83561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:1960; CHRNA7.
MIM; 118511; -.
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58
134
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490
164
213
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262
296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYHHHDPDGGKMPKWTRVVLLNWCAWFLRMKRPG-----EDKVRPACQHNERRCS--LAS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELKE-RSSKSLLANVLDIDDDFR----HNCRPMTPGGTLPHNPAFYRTVYGQGDDGSI- 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVV 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 VCLAGYHEKRLIHDILDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 KLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQTNVVVRNNGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 LYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGGDISSYVLNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WELLGVPGKRNEIYYNCCPEPYIDITFAIIRRRTLYYFFNLIIPCVLIASMALLGFTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 WDLVGVLGKRSEKFYECCKEPYPDVTFTVSIRRRTLYYGLNLLIPCVLISALALLVFLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                           NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                         ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).

(BY SLINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

Missing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 499;
                                                                                                                                  InterPro; IPR006202; Neur_channel memb.
InterPro; IPR006202; Neur_channel memb.
InterPro; IPR006202; Neur_channel.
Pfam; PF02931; Neur_chan_IBD, 1.
Pfam; PF02932; Neur_chan_IBD, 1.
PRINTS; PR00252; NRIONCHĀNNEL.
TIGRFĀMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.
POSTSYNABPLIC membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1157; DB 1; Length 49
Pred. No. 3e-73;
5; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56002 MW; AEE5D0B3820D42D5 CRC64;
                                                                                                                                                                                                                                                                                                         ALPHA-7 CHAIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEMSAVAGPPATNGNLLYI--GFRGLDTMHCAP-TP-
                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.6%; SCOJ
46.4%; Pred
ative 76;
                                                                                                                          EMBL; X93604; CAA63802.1; -.
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405 GRVACSPTHDEHLLHAGQPSEGDPDLAKILEEVRYIAHRFRCQDESEAVCSEWKFAACVV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
STRAIN=Bristol N2;
Ballivet M., Alliod C., Bertrand S., Bertrand D.;
"Nicotinic acetylcholine receptors in the nematode Caenorhabditis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMEL; X33887; CAA58764.1; -..
RMEL; AF022973; AAC25796.1; -..
RPIR; G65888; G6588.
RHSSP; F58154; 119B.
RHCFPC; IFRO06029; Neur Channel memb.
RITHEFPC; IFRO06029; Neur Channel memb.
RITHEFPC; IFRO06201; Neur Channel.
RPfam; PF02931; Neur Channel.
RPfam; PF02932; Neur Channel.
RPfam; PF02932; Neur Channel.
RPfam; PF02932; Neur Channel.
RPfam; PF02932; Neur Channel.
RPfam; PF02932; Neur Channel.
RPfam; PF02932; Neur Channel.
RPTGRFAM; TIGR00860; LIC; 1.
RPGRFAM; TIGR00860; LIC; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
RROSITE; PS00234; NEUROTRIONECHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - FUNCTION: Possible acetylcholine receptor.
- SUBCELLULAR LOCATION: Integral membrane protein.
- SIMILARITY: Belongs to the ligand-gated ionic channel family.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                    28-FBB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor like protein, alpha-type chain precursor.
F2SG6.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Bristol N2;
Nelson J., Wohldmann P.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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BY SIMILARITY.
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(Rel. 33, Last sequence update)
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J. Mol. Biol. 258:261-269(1996)
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           (POTENTIAL)
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Bossy B., Ballivet M., Spierer P.;
"Conservation of neural nicotinic acetylcholine receptors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACHI DROME STANDARD; PRT; 567 AA.

P09478; 034074;
01-MAR-1989 (Rel. 10, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
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                                                                    27.3%; Score 43.3%; Pred. No. 1.5e-v., 43.3%; Pred. No. 1.5e-v., 76; Mismatches 139;
     N-LINKED (GLCNAC.
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                            498 AA;
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Maniki. Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baddwin D.,
RA Ballew R.M., Basen A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Bernan B.P., Brokstein D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavaley S., Dahlke C., Davenport L.B., Davies P. D.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J. Evangelista C.C., Ferrac C., Ferrac B., Punkov B.C., Dunn P.,
RA Durbin K.J. Evangelista C.C., Ferrac C., Ferrac B., Flasser K.,
RA Durbin K.J. Evangelista C.C., Rerac C., Ferrac B., Flasser K.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Heiman T.J., Mein M.H., Ibegwam C.,
RA Harris N.L., Harvey D.A., Heiman T.J., Mein M.H., Ibegwam C.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Harris M.,
RA Lasko P., Lei Y., Levitsky A.A., Liu J.H., Ibegwam C.,
RA Liu X., Matteri B., McIntcoh T.C., McLeod M.P., Moshrefi A.,
RA Liu X., Matteri B., McIntcoh T.C., McLeod M.P., Moshrefi A.,
RA Liu X., Matteri B., McIntcoh T.C., McLeod M.P., Pachleb J.M.,
RA Balazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,
RA Reinert K., Slden-Kiamos II., Slmpson M., Strong R., Sun E.,
RA Reinert X., Wassarman D.A., Wenner S., Wang A.H., Wang X.,
RA Bang Z.-Y., Wassarman D.A., Wenner J.C.,
RA Wang Z.-Y., Wassarman D.A., Walner G.W., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Walner G.C., Zhan M., Zhang G., Zhao Q., Zhan G.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleron M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
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"Annotation of the Drosophila melanogaster euchromatic genome: systematic review.";

by an and Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
-!- FUNCTION: After binding acetylcholine, the AChR responds by extensive change in conformation that affects all subunits leads to opening of an ion-conducting channel across the pl

SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: CNS in embryos. -!- DEVELOPMENTAL STAGE: Late embryonic, late pupal and second instar -!- SIMILARITY: Belongs to the ligand-gated ionic channel family. larvae stages

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; AE003747; AAF56301.2; -. S00381; ACFFA1. EMBL; X07194; CAA30172.1;

Flysse; FBgn0000036; nAcR-alpha-96Aa. InterPro; IPR006029; Neu channel memb. InterPro; IPR006202; Neur_chan LBD. InterPro; IPR006201; Neur_channel.

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                                              TICRFAMS; TICRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane; Multigene family; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                     ALPHA
                                                                                                                                                                                                                                                                                    ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
Y -> H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 168; Indels 102;
                                                                                                                                     PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                              22.0%; Score 888; DB 1; Length 567; 35.2%; Pred. No. 2e-54;
                                                                                                                                                                                                                                                                                                                                                                              -> H (IN REF. 1).
08E1F721FB2A92AC CRC64;
                                                                                                                                    ACETYLCHOLINE RECEPTOR
LIKE CHAIN 1.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                            -> H.
-> H (IN REF.
                                                                                                                                                                                                                                                                      BY SIMILARITY
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                 Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
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223
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272
3306
3326
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TRANSMEM
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516 AA

PRT;

STANDARD;

RESULT 8 ACH1 MANSE ID ACH1_MANSE

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                                                                                                       Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor; Postsynaptic membrane; In Transment; Glycoprotein; Signal; Transmembrane; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                insect Manduca sexta.";
Eur. J. Neurosci. 10:879-889(1998).
-:- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
                  01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-like chain precursor (MARA1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ligand-gated ionic channel family.
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BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98424077; PubMed=97531155;
Bastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
"Characterization of a nicotinic acetylcholine receptor from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 516;
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Y09795; CAA70928.1;
InterPro; IPR006029; Neu Channel memb.
InterPro; IPR006202; Neu Chann.EBD.
InterPro; IPR006202; Neur Chan LBD.
InterPro; IPR006201; Neur Chan LBD.
Pfam; PF02931; Neur Chan EBD; 1.
PRINTS; PR00252; Neur Chan memb; 1.
PRINTS; PR00252; NRTONCHANNEL.
IIGREAMS; TIGR00866; LLC; I.
PROSITE; PS00236; NEUROTR, ION CHANNEL; 1.
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01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
28-FEB-2003 (Rel. 41,
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233
516 AA;
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Best Local Similarity
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ACH2 HUMAN STANDARD;
Q1582; Q9HAQ3;
01-NOV-1997 (Rel. 35, Created)
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ACH2_HUMAN
ID ACH2_HI
AC Q15822;
DT 01-NOV-
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                              128 KATLNYTGRVEWRPPAIYKSSCEIDVEYFPFDQQTCVMKFGSWTYDGFQVDLRHIDEVRG 187
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    415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDBTGG
                                                                                                                                                                      II PCVLIASMALLGFTLPPDSGEXLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
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                                                                                       -----DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFALIIRRTLYYFFNL
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-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
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Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
                                                                                                                                                                                                                                                                                                 308 LFTMILDTFSICVTVVVLAVHFRSPQTHTMSPWVRRVFIHVLPRLLVMRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylohilm receptor protein, alpha-Li chain precursor.
Schistocerca gregaria (Desert locust)
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InterPro; IPR006029; Neu_channel_memb.
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                 INCERTO; IRNOVAZAI; NEUT CHAN IBD; 1.
Pfam; PF0231; Neut Chan IBD; 1.
Prim; PF02923; Neut Chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUKOTR ION CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1 CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 YLLFTMVLVGLSVVITIMVLNVHYRKPSTHKMAPWVRKVFIRRLPKLLLMRVPEQLL---
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N-LINKED (GLCNAC.
ALA/SER-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                              21.6%; Score 873; DB 1;
36.8%; Pred. No. 2.2e-53;
iive 90; Mismatches 174;
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                                                                                                                                                                                  EXTRACELLULAR
                                                                                                                                                                                                                                               CYTOPLASMIC.
                                                                                                                                       POTENTIAL
IPR006202; Neur_chan_LBD IPR006201; Neur_channel.
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                                                                                                                  Transmembrane; Multigene family
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R GO; GO:005892; C:nicotinic acetylcholine-gated receptor-chan. ..; TAS.

R GO; GO:0015464; F:acetylcholine receptor activity; TAS.

R GO; GO:0015464; F:nicotinic acetylcholine-activated cation-se. ..; TAS.

R GO; GO:0007165; P:nicotinic acetylcholine-activated cation-se. ..; TAS.

R GO; GO:0007165; P:nignal transduction; TAS.

R GO; GO:0007165; P:nignal transduction; TAS.

InterPro; IPR006202; Neur channel memb.

InterPro; IPR006202; Neur channel.

R Fram; PF0231; Neur channel.

R Pfam; PF0232; Neur channel.

R Pfam; PF0232; Neur channel.

R Pfam; PF0232; Neur channel.

R Pfam; PF0232; Neur channel.

R TIGRFAMS; TIGNCHANNEL.

R PRINTS; PR00225; NEURONTE ION CHANNEL; 1.

R POSTEN; PS00236; NEURONTE ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBGNAT: Neuronal AChR seems to be composed of two different types of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be combined to beta-2 or beta-4 to give rise to functional receptors.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                MEDLINE-197062879; PubMed=8906617; Berckhan K.J., Urrutia A., Ellis S.B., Berckhan K.J., Urrutia A., Ellis S.B., Berckhan K.J., Urrutia A., Ellis S.B., Berckhan K.J., Urrutia A., Ellis S.B., Berckhan K.J., Urrutia A., Harpold M.M.; Camparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional beta 4 subunits."; beta 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";
                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                    28-FEB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Groot Kormelink P.J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPHA-2 CHAIN.
EXTRACELLULAR.
   01-NOV-1997 (Rel. 35, Last sequence update)
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CYTOPLASMIC
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EMBL; AF311103; -; NOT ANNOTATED_CDS.
Genew; HGNC:1956; CHRNA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U62431; AAB40109.1; -.
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289
315
352
502
                                                                      Homo sapiens (Human)
                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                     TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                    SEQUENCE FROM N.A.
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297
331
353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 VHHRSPSTHTMPHWVRGALLGCVPRWLLMNRPPPVVEL---CHPLRLKLSPSYHWLESNV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629 ELKERSSKSLLANVLDIDDDFRHNCR-PMTPG-GTLPHNPAFYRTVYGQGDDGSIGPIGS
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                                                                                                                                                                                                                                                                                                     53 GSHTETEDRIFKHLFRGYNRWARPVPNTSDVVIVRFGLSIAQLIDVDEKNQMMTTNVWLK
                                                                                                                                                                                                                                                                                                                                              366 LEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCL
                                                                                                                                                                                                                                                                                                                                                                       309 GYH---EKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEKNQLLVTNVWLK
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH3 HUMAN STANDARD; PRT; 503 AA.
P32297; Q15823; Q96RH3; Q99553; Q9RQ93;
01-0CT-1993 (Rel. 27, Created)
01-0V-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
        BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                         ASCULALLE

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

**-*:TINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90245296; PubMed=2336208; Fornasari D., Chini B., Tarroni P., Clementi F.; "Molecular cloning of human neuronal nicotinic receptor alpha
                                                                                                                                                                                      21.0%; Score 848.5; DB 1; Length 529; 36.7%; Pred. No. 1e-51; ive 87; Mismatches 154; Indels 75;
                                                                                                                             A -> T (IN REF. 3).
7F512B06CCD9AAFD CRC64;
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SEOUENCE FROM N.A. (ISOFORM 1).
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129 1
235 2
125 1
529 AA;
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A Strausberg R.L., Feingold E.A., Grouse I.H., Derge J.G.,
Atlausner R.D. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altaschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeares M.B., Mang J., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B Evomstein M.J., Usdin T.B., Toshiyuki S., Carninci D., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
B Richards S., Worley K.C., Hale S., Garcia A.M., Gable B.H.,
R Hahey J., Helton B., Ketteman M., Madak M.A., Gabbs R.A.,
R Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M.,
B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
R "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=97162233; PubMed=9009220;

Groot Kormelink P.J., Luyten W.H.M.L.;

"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAchR) subunits beta3 and beta4 and expression of seven nAchR subunits in the human neuroblastoma cell line SH-SYSY and/or IMR-32.";

FEBS Lett. 400:309-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99118870; PubMed=9921897; Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.; "The structures of the human neuronal nicotinic acetylcholine receptor beta2- and alpha3-subunit genes (CHRNB2 and CHRNB3)."; Hum. Genet. 103:645-653(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
MEDLINE=21342809; PubMed=11450844;
MEDLINE=21342809; PubMed=11450844;
Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.,
"Characterization of the human beta4 nAChR gene and polymorphisms in CHRNB3 and CHRNB4.";
                                                                     coding for the alpha 3 subunit
                                                                                                                                                                     MEDLINE=97062879; PubMed=8906517;
Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
Chavez-Noriega L.E., Johnson B.C., Velicelebi G., Harpold M.M.,
"Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
beta 4 subunits.",
J. Mol. Neurosci. 7:217-228(1996).
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TISSUE=Epidermal keratinocytes;
Arredondo J., Grando S.A.;
"Cloning cholinergic receptors in human keratinocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Brain;
Anand R., Lindstrom J.;
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                        Mihovilovic M., Roses A.D.,
"Expression of mRNAs in human thymus coc
of a neuronal acetylcholine receptor.",
                      MEDLINE=91114756; PubMed=1989896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISOFORM 2)
                                                                                                           Exp. Neurol. 111:175-180(1991)
                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2)
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DR GO; GO:0005892; C:nicctinic acetylcholine-gated receptor-chan. ..; TAS.

DR GO; GO:00015464; F:acetylcholine receptor activity; TAS.

DR GO; GO:00015464; F:acetylcholine receptor activity; TAS.

DR GO; GO:000155; F:transporter activity; TAS.

DR GO; GO:000155; F:stansporter activity; TAS.

DR GO; GO:000165; P:stansport; TAS.

DR GO; GO:0006810; P:transport; TAS.

DR InterPro; IPR006029; Neur chan LBD.

DR InterPro; IPR006020; Neur chan LBD.

DR PROS; DR PRO05021; Neur chan memb; 1.

DR PRIMTS; PR00522; NRICNCHĀNNEL.

DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.

DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.

MR Receptor; Postsynaptic membrane; Indic channel; Glycoprotein; Signal; W Transmembrane; Multigene family; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .; TAS.
                                                                            -!- SUBUNIT: Neuronal AChR seems to be composed of two different type
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PÔTENTIAL.
NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                         Note=No experimental confirmation available; SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED WITH RECEPTOR ACTIVATION
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                                                                                            of subunits: alpha and non-alpha (betA).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALPHA-3 CHAIN.
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                                                            IsoId=P32297-1; Sequence=Displayed;
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EMBL, AJ007784; CAR07682.1; -
EMBL, AJ007785; CAR07682.1; JOINED.
EMBL, AJ007785; CAR07682.1; JOINED.
EMBL, AJ007786; CAR07682.1; JOINED.
EMBL, BC001642; ARH01642.1; -
EMBL, BC002096; ARH02296.1; -
EMBL, BC000513; ARH0513.1; -
EMBL, RA385584; AAK68110.1; -
EMBL, X53559; CAR37625.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                  M37981, AAA59942.1; -. U62432, AAB40110.1; -. Y08418; CAA69695.1; -.
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PIR; A53956; A53956.
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                                                                                                                                                                                               295 ILIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 NAQKPRPLYGAELSNINCFSRAES------KGCKEGYPCQDGMCGYCHHRRIKISNF 413
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                                                                                                                                                                                                             355 NOLLVINVWIKLEMNDMNIRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                              415 NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
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                                                                                                                                                                                                                                                                                                                                                                                               SMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-50301489; PubMed-2114015;
Baumann A., Jonas P., Gundelfinger E.D.;
"Sequence of D alpha 2, a novel alpha-like subunit of Drosophila
                                                                                                                                                                       64;
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P17644; Q9VC73;
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acctylcholine receptor protein, alpha-like chain 2 precursor.
NACR-ALPHA-96AB OR ACRE OR SAD OR ACR96AB OR CG6844.
                                                (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 6
                                                                                                                                              Score 845; DB 1; Length 503;
                                                                                                                                                                       97; Mismatches 166; Indels
MGSGPL (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 ISIVITVFVLNVHYRTPTTHTMPSWVKTVFLNLLPRVM------
                                                                                                                       8A9EBC5D71AEC7D6 CRC64;
                                               VSLPLALSP -> ALAAPGAVA
LSPP -> CRA (IN REF. 1).
D -> G (IN REF. 1).
                                                                                                -> S (IN REF. 1).
                                                                                                                                                           1.7e-51;
                                                                                   DD -> TT (IN REF.
           /FTId=VSP_000073.
                        L -> LL. _
/FTId=VAR_013240.
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                                                                                                                                                            Pred. No.
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                                                                                                                          57309 MW;
                                                                                                                                                 20.9%;
35.2%;
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RINGLE GECYLCHOLINE RECEPTOR: 1,

Nucleic Acids Res. 18:3440-3640(1990).

RINGLESS CAGES RES. 18:3440-3640(1990).

RINGLESS CAGES RES. 18:3440-3640(1990).

RINGLESS CAGES CAGES TO PROBE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE CAGES TO THE C
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMSL openantics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 HSW-----IFLLIYLNLSAKVCLAGYHEKRLLHDLLDPXNTLERPVLNESDPLQLSFGLT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DL----QLQD-----ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQL 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 SLALPLIGKYLLFTMLLVGLSVVITIIILNIHYRKPSTHKMRPWİRSFFIKRLPKLLIMR 377
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                                                                                                                                                                                                                                                                         PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Receptor; Postsynaptic membrame; Ionic channel; Glycoprotein; Signal;
Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----WIRIVFLCWLPWILRMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                   ACETYLCHOLINE RECEPTOR PROTEIN, ALFHA-
LIKE CHAIN 2.
EXTRACELLULAR (POTENTIAL).
                      DEVELOPMENTAL STAGE: Late embryonic and late pupal stages. SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
97D6A46CADC3F42F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 2.6e-51;
87; Mismatches 170; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 576;
    membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.9%; Score 843.5;
SUBCELLULAR LOCATION: Integral memb
TISSUE SPECIFICITY: CNS in embryos.
DEVELOPMENTAL STAGE: Late embryonic
                                                                                                                                                                                              InterPro; IPR006629; Neu channel memb.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur channel.
                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                      FlyBase; FBgn0000039; nAcR-alpha-96Ab.
                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                         PROBABLE.
                                                                                                                                                                                                                               Pfam; PF02931; Neur chan_LBD; 1.
Parm; PF02932; Neur chan_memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                        AE003748; AAF56303.1; -. AY058446; AAL13675.1; -.
                                                                                                                                    EMBL; X52274; CAA36517.1; -.
EMBL; X53583; CAA37652.1; -.
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193; Conservative
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254
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293
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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holf R.A., Hoskins R.A., Galle R.F.,
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Ruttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                       410 MOMNSGGSSPDSLRRMOGRVGAGGCNGMHVTTATNRFSGLVGALGGGLSTLSGYNGLPSV 469
599 RPGRPLILEFPTTPCSDTSSERKHQILSDVELKE----RSSKSLLANVLDIDDDFRHNC 653
                                                                                                                                                                                                                                                                                                                                                                                               470 LSGLDDSLSDVAARKKYPFELEKAIHNVMFIQHHMQRQDEFNAEDQDWGFVAMVMDRLFL 529
                                                                                                                                                                        --TRMPDA
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                                                                                        ---KDLLRDLAANKINYGLKFSKTKFGQAL-MDE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hermans-Borgmeyer I., Zopf D., Ryseck R.-P., Hovemann B., Betz H.,
Gundelfinger E.D.;
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MEDLINE=88174720; PubMed=2832736;
Wadsworth_S.C., Rosenthal L.S., Kammermeyer K.L., Potter M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACHS JKOME
PD4755; Q9VZC3;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
10-OCT-2003 (Rel. 42, Last amnotation update)
ACCT-2003 (Rel. 42, Last amnotation update)
NACR-BETA-64B OR ACRO OR ARD OR ACR64B OR CG11348/CG12606.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Behydroidea; Edopterygota; Diptera; Brachycera; Muscomorpha;
NNGD1_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of a developmentally regulated nicotinic
                                                                                                                                                                            -DGSIGPIGS-
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EMBO J. 5:1503-1508(1986),
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MEDLINE=20196006; PubMed=10731132;
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A Hostin D., Houston K.A., Howland T.J., Hermandez J.R., Houck J.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lux X., Mattei B. McIntosh T.C., McLood M.E., Moshrefi A.,

RA Lux X., Mattei B., McIntosh T.C., McLood M.E., Moshrefi A.,

RA McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Molson D.R., Nelson K.M., Nixon K., Nixon D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shire B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Stirskas R.Y. Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng R., The Globs R.A., Myers B.W., Rubin G.M., Venter J.C.;

RY The Globs R.A., Myers B.W., Rubin G.M., Venter J.C.;

RY The Globs R.A., Myers B.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flyase; Person Control of the Channel memb.
InterPro; IPR006029; Neu_channel memb.
InterPro; IPR006202; Neur_chan LBD.
InterPro; IPR006201; Neur_chan LBD.
InterPro; IPR006201; Neur_chan LBD, 1.
Pfam; PF02931; Neur_chan memb; 1.
Pfam; PF02932; Neur_chan memb; 1.
PRINTS; PR00252; NEUROHANNEL.
IIGREAMS; TIGR00860; LIC; I.
PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000).
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: CNS in embryos.
-!- DEVELOPMENTAL STAGE: Late embryonic and late pupal stages.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLCHOLINE RECEPTOR PROTEIN, CHAIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X07956; CAA30778.1; -:
EMBL, X07957; CAA30778.1; JOINED.
EMBL, X07958; CAA30778.1; JOINED.
EMBL, X0316; AAA28311.1; -:
EMBL, AE003481; AAF47900.1; -:
PIR; S03012; ACFFNN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; Postsynaptic membrane;
Transmembrane; Multigene family.
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521 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCSDTSSERKHQILSDVELKERSS----KSLLANVLDIDDDFRHNC---RPMTPGGTLPH 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 -----GLGD----GCRRESESSDSILLSPEASKATE-----AVEFIAEHLRNE 462
                                                                                                                                                                                                                                                                                  DETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEP-YIDITFAIIIRRRTLYYFFNLII 528
                                                                                       665 NPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTBYBLGLILKEIRFITDQLRKD
                                                                                                                                                                                                           411 TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQL-Q
                                                                                                                                                                                                                                                                                                          PGMSMPAHPHPSYGSPAELPKHISAIGGKOSKMEVMELSDLHHPNCKINRKVNSGGEL--
                                                                                                                                        351 VDEKNQLLVTNVWLKLEWNDMNLRMNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                            ----DAVPLWIRIVFLCWLPWILRMSRPGRPLILEFPTT
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-88223624; PubMed=3267226;

Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.;

"Genes expressed in the brain define three distinct neuronal

nicotinic acetylcholine receptors.";

EMBO J. 7:595-601(1988).

-!- FUNCTION. After binding acetylcholine, the AChR responds by an

extensive change in conformation that affects all subunits and
leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Neuronal AChR seems to be composed of two different type of subunits: alpha and non-alpha (also called beta). A functional receptor seems to consist of two alpha-chains and three non-alpha chains.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the ligand-gated ionic channel family.
                               70;
Length 521;
                                                                                                                                                                                                                                                                                                                                                         PCVLIASMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLYIQTREDWKYVAMVIDRLQLYIFFIVTTAGTVGILMDAPHI 505
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHI
20.8%; Score 840; DB 1; 35.6%; Pred. No. 3.9e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528 AA
                                 95; Mismatches
 Query Match 20.8°
Best Local Similarity 35.6°
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMID outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEKNOLLVINVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 TGGDISSYVLNGEWELLGVPGKRNELYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCV 531
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LISCLTVLVEYLPSDCGEKITLCISVLLSLTVFLLLITEIIPSTSLVIPLIGEYLLFTMI 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 WCFVTLQAATREQKQPHGFAEDRLFKHLFTGYNRWSRPVPNTSDVVIVKFGLSIAQLIDV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EFPTTPC----SDISSERKHQILSDVELKERSSKSLLANVL---DIDDDFRHN 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 YQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 HHVDLKDYWESGEWAIINAIGRYNSKKYDCCTEIYPDITFYFVIRKLPLFYTINLIIPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL------
                                                                                                                                                                                                                                                                                                                                                                                                 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 5.5e-51;
81; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E76C6360AF876364 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%; Score 838;
                                                                                                          EMBL; X07339; CAB55645.1; --
EMBL; X07340; CAB59645.1; --
EMBL; X07341; CAB59645.1; JOINED.
EMBL; X07342; CAB59645.1; JOINED.
EMBL; X07343; CAB59645.1; JOINED.
EMBL; X07344; CAB59645.1; JOINED.
EMBL; X07344; CAB59645.1; JOINED.
EMBL; AJZ50360; CAB59645.1; JOINED.
EMBL; AJZ50360; CAB59625.1; --
PIR; S00377; ACCH2N.
InterPro; IPR006029; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
Ffam; PF02931; Neur_chan_LBD; 1.
PERMYS; PR00252; Neur_chan_memb; 1.
PRINYS; PR00252; Neur_chan_memb; 1.
PRINYS; PR00252; Neur_chan_memb; 1.
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528 AA;
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SEQUENCE
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371 YDPPGTRLSTSRCWLETDVDDKWEEEEEEEEEEEEEEEKAYPSRVPSGGSQGTQCHYS 430
                                              709
                                                                                  467
                                        CRPM---TPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGL
                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A., Ray N., Raftery M.A.; "Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Pentamer of two alpha chains, and one each of the beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klarsfeld A., Daubas P., Bourachot B., Changeux J.-P.;
"A 5'-flanking region of the chicken acetylcholine receptor alpha-
subunit gene confers tissue specificity and developmental control c
expression in transfected cells.";
Mol. Cell. Biol. 7:951-955(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           delta, and gamma chains.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                         LIKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-84206570; PubMed-6327170;
Ballivet M., Nef P., Stalder R., Fulpius B.;
"Genomic sequences encoding the alpha-subunit of acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M., "Genes expressed in the brain define three distinct neuronal micotinic acetylcholine receptors.";
EMBO J. 7:595-601(1988).
                                                                            CEROAGKASGGPAPQVPLKGEEV---GSDQ-----GLTLSPSILR-
                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cold Spring Harb. Symp. Quant. Biol. 48:83~87(1983)
                                                                                                                                                                                                                                                          456 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 21-44.
MEDLINE=85270494; PubMed=3860855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88283624; PubMed=3267226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87144271; PubMed=3821734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-12 FROM N.A.
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DR EMBL; X07330; CAA30282.1; -.

DR EMBL; X07331; CAA30282.1; JOINED.

DR EMBL; X1243; CAA30282.1; JOINED.

DR EMBL; X12435; CAA30282.1; JOINED.

DR EMBL; X12435; CAA30282.1; JOINED.

DR EMBL; X07331; CAA30282.1; JOINED.

DR EMBL; X07335; CAA30282.1; JOINED.

DR EMBL; AP051909; AAC06012.1; -.

DR EMBL; MA1809; AAA4865.1; -.

DR EMBL; MA1809; AAA4865.1; -.

DR EMBL; MA1809; NAA4865.1; -.

DR EMBL; MA1809; NAA4865.1; -.

DR PIR; 150150; 150150.

DR PIR; S00075; Neur_chanlel memb.

DR InterPro; IPR006202; Neur_chanlel.

DR InterPro; IPR006202; Neur_chanlel.

DR PF02931; Neur_chanlel.

DR PF02932; Neur_chanlel.

DR PF02932; Neur_chanlel.

DR PGMTS; PS00236; NEUROTR ION CHANNEL; 1.

DR PRINTS; PS00236; NEUROTR ION CHANNEL; 1.

DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.

DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.

FT SIGNAL

FT SIGNAL

TCARRAMS; TICROBORO; LIC; 1.

THE SIGNAL

TRANSMENTANEL POSESYNAPTIC membrane; Ionic channel; Signal; FT CHAIN 21 456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
20.5%; Score 827.5; DB 1; Length 456;
Best Local Similarity 34.6%; Pred. No. 2.4e-50;
Matches 176; Conservative 92; Mismatches 130; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (PROBABLE)
E -> D (IN REF. 4).
0B31B6EABD7B4D42 CRC64;
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Search completed: May 7, 2004, 11:36:31 Job time : 16.3803 secs us-09-303-232-2.rspt

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 11:30:03; Search time 48.3701 Seconds (without alignments) 5022.709 Million cell updates/sec May Run on:

US-09-303-232-2 4043 1 MKNAQLKLTEVDDDELWLAV.....MFAILATIAVLLSAPHIIVS 770 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

1017041 Total number of hits satisfying chosen parameters: 1017041 seqs, 315518202 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL 25:* Database :

sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_phage:*
sp_phage:*
sp_phage:*
sp_phage:*

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	O8t7v5 drosophila		08t5f5 drosophila		_		_		O86mn8 drosophila		_	_	_	O9nkd2 drosophila	-	~
SUMMARIES		ID	Q8T7V5	6TCV6Q	OSTSFS	Q86MIN7	6IMA60	Q9XZI3	Q8T7.52	Q8T7S3	Q86MN8	Q8T7S1	Q8T7R9	Q9XZI4	Q8T7S0	Q9NKD2	Q9VL79	Q8IPE2
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		Score	4014.5	2613	2388.5	1991	1988	1850	1625.5	1622.5	1621.5	1620.5	1611	1609	1602	1502	1310.5	1235
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                                                                                                                                           Gaps
                                                                                                                                           37;
                                                                                                             5; Length 807;
             TIGRPAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Fostsynaptic membrane; Receptor;
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                                                                             C8B4F6B34287C8C8 CRC64;
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                                                                                                             Score 4014.5;
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PRT;

O9VJT9; 01-MAY-2000 (TrEMBLrel. 13, Created)

PRELIMINARY;

QPUJT9

RESULT 2 Q9VJT9

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SEQUENCE FROM N.A.

Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
A Brandon R.C., Rogers Y.H., Elazel, R.G., Champe M., Pfelffer B.D.,
A Burdon R.C., Rogers Y.H., Elazel, R.G., Champe M., Pfelffer B.D.,
A Barndon R.C., Rogers Y.H., Elazel, R.G., Champe M., Pfelffer B.D.,
A Barndon R.C., Rogers Y.H., Elazel, R.G., Champe M., Pfelffer B.D.,
A Barndon R.C., Rogers Y.H., Elazel, R.G., Champe M., Pfelffer B.D.,
A Barndon R.C., Rogers Y.H., Elazel, R.G., Champe M., Pfelffer B.D.,
Ballew R.M., Baros P.V., Berman B.P., Bandari D., Botchan D.,
Ballew R.M., Cawles D.A., Butler H., Cadieu E., Center A., Chandra I.
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.
Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Diezz S.M.,
Carry J.M., Cawley S., Dallker C., Dewroport L.B., Davitas P.,
Burtis K.C., Erazel C., Ferrac C., Ferrica S., Pleischman W.,
R. Gong F., Gorrell J.H., Qu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Gann P., Harris M.,
A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Gann B.,
A Hostin D. Houston K.A., Howland T.J., Weilmison J.A., Metchum K.A.,
Bandolek A., Mong F., Karpen G.H., Ke Z., Kannison J.A., Metchum K.A.,
Bandolek M., Muthy B., Murphy L., Muzny D.N., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Parl W., Nelson D.L.,
Rak Reinert K., Remington K.A., Saunders R., Soneler F., Shen H.,
Shier B., Spradling A.C., Stapheton M., Stupski M.P., Santh T.,
Spier B., Spradling A.C., Stapheton M., Stupski M.P., Santh H.O.,
Rateng X.H., Zhong W., Wuthy W., Wuther B., Shong S., Yao Q.A., Yang S., Thu K., Shong W., Wuthy W., Wuthy W., Wuthy W., Walsenbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, ARF030462; AFF3374-3; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
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                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota, Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha; Ephydroida, Drosophilidae, Drosophila.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
24,
                                                                                                        NACRALPHA-34E OR CG32975.
(TrEMBLrel. (TrEMBLrel.
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GO; GO:0030594; F:neutocrams

R GO; GO:0006811; P:ion transport; IEA.

R InterPro; IPR006202; Neur chan LBD.

R InterPro; IPR006202; Neu chan LBD.

R Pfam; PF02931; Neur chan LBD. 2.

R Pfam; PF02932; Neur chan LBD. 2.

R PRIMTS; PR00252; NEUCHANNEL.

DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.

SO SEQUENCE 570 AA; 64767 MW; DBB21E1E185263BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor activity; IEA
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                                                                                                                                                                                                                                 64.6%; Score 2613; DB 5;
69.0%; Pred. No. 1e-219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 GFTLPPDSGEKLSLGT----YFNCIMFMVASSVVSTI
                                                                                                                                                                                                                                                                       17; Mismatches
                                                                                                                                                                                                                    Query Match
Best Local Similarity 69.0°
Matches 532; Conservative
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Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on R
Mediated A-to-I Pre-mRNA Editing.",
Genetics 160:1519-1531 (2002).
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01-JUN-2002 (TrEMBLrel. 21, last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalphas subunit.
NACR-ALPHA-34E OR NACRALPHA34E OR BG:DS05899.4 OR BG:DS05899.5 (
CG4498 OR CG16878 OR CG32975.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
11 TaxID=7227;
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Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----WIRIVELCWLPWILRMSRPGRPLILEFPTTPCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLIY---LNESAKVCLAGYHEKRLIHDLIDPYNTLERPVLNESDPLQLSFGLTLMQIIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                          Millar N.S.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ554210.
GO, GO:0016020; C:membrane; IEA.
GO; GO:00160230; F:extracellular ligand-gated ion channel acti.
GO; GO:001031094; F:neurotransmitter receptor activity; IEA.
GO; GO:0010811; P:ion transport; IEA.
InterPro; IPR066201; Neur_channel.
InterPro; IPR066202; Neur_chan_IBD.
InterPro; IPR066202; Neur_chan_IBD.
Pfam; PF02931; Neur_chan_IBD.
Pfam; PF02931; Neur_chan_IBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroida; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                   01-0UN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor subunit Dalpha7 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.2%; Score 1991; DB 5; Length 54; 72.8%; Pred. No. 2.7e-165; ive 43; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69D2C39746BB74D7 CRC64;
                                           542 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR ION_CHANNEL; 1.
                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 AA; 60988 MW;
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                                              PRELIMINARY;
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542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Receptor.
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MEDINTS-2018006; Broked-10/31124;

RA Adams M.D., Celniker S.E., Holt R.A., Bvans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Retron G.G., Worthand J.R., Yandell M.D., Zlang Q., Chen L.X., Ratton G.G., Worthand J.R., Yandell M.D., Zlang Q., Chen L.X., Ratton G.G., Worthand J.R., Yandell M.D., Zlang Q., Chen L.X., Ratton G.G., Worthand J.R., Hazej R.G., Chango M., Miklos G.L.G., Abrit J. P. Botchan M. M. Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ratlur R.M., Basu A., Baxendala J., Bayraktaroglu L., Basaley E.M., Beeson K.Y., Bence P.V., Barnan B.P., Bhandari D., Bolahakov S., Bortchan M.R., Bouch J., Botchan M.R., Bouch J., Botchan M.R., Bouch J., Cadieu B., Center A., Charler P., Ra Hurtis K.C., Busam D.A., Dahlke C., Davemport L.B., Davier P., Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davier S.P., Ra Dodson K., Doup L.B., Doubler A., Dany E., Gargell S., Markov B.C., Dunn P., Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davier S.M., Goos K., Doup L.B., Daviers M., Davier M.M., Glasser K., Goog K., Gorrell J.H., Gu Z., Gana P., Harris M., Alase R., Goog F., Lei Y., Harvey D., Heiman T.J., Herrandez J.R., Harris M., Hostin D., Houston K.A., Halvey D., Heiman T.J., Herrandez J.R., Harris M., Laskov D., Heiman T.J., Wei M.-H., Ibeeyam C., Lask M., Mallah R., Kalpen G.H., Ke Z., Kennigton J.A., Ketchum K.A., Jalli M., Kalush F., Karpen G.H., Ke Z., Kennigton J., Lin X., Liang Y., Lin X., Atten G.D., Kraft C., Mozris J., Mozhry D., Lin X., Marteri B., Mourt S.M., Moy M., Murphy B., Murphy L., Muzskern D.M., Nelsen H., Ralazzolo M., Pittum G.S., Pan S., Pollard J., Pull Y., Pacles M. G., Shen H., Ryineas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinsten M., Shung A.H., Wang X., Ye J., Ye R., Woods T., Wassarman D.A., Wallenber C., Shang G.M., Wang G.L., Wang G.L., Shang G.M., Wang G.L., Wang G.L., Shang G.M., Wang G.L., Wang G.L., Shang M., Wang Z.-Y., Wassarman D.A., Weinsten M., Wang G.L., Wassarman D.A.,
435 MYRQGDDGSVGPVGPAGPVVDGRLHEAIS-HTCLTSSAEYELALILKELRWITEQLKKED 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Evans C.A., Gocayne J.D., Amanatides P.G., Breson K.Y., Busam D.A.,
Banzon J.A., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,
Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG32538 protein.

NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.

Drosophila melanogaster Fruit fly,

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                            726 ECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      545 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=7227;
                                                                                                                                                                                               494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9VWI9;
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                                                                                                                                                                                                                                                                                                                                      RESULT 5
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7102;
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                                                                                                                                                                                                                 S 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDMNLRWNSSEFGGVRDLRIPPHRLWK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDVLMYNSADEGFDGTYAINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLQLSFGLTLMQIIDVDEKNQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWIYDGFQLDLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRRILYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPAT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --WIRIVFLCWLPWILRMS 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPGRPLILEFPTTPCSDTSS---BRKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRP 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                              Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smithiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Photanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003511; ARF48950.2; -.

R PlyBase; FBG0031014; nAcR-alpha-18C.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:001605230; F:neurotransmitter receptor activity; IEA.

R GO; GO:0005230; F:neurotransmitter receptor activity; IEA.

R GO; GO:0005230; F:neurotransmitter receptor activity; IEA.

R GO; GO:000694; F:neurotransmitter receptor activity; IEA.

R GO; GO:000691; P:neurotransmitter receptor activity; IEA.

R GO; GO:000601; Neur chan LBD.

R InterPro; IPR006029; Neur chan LBD.

R PROMOFO291; Neur chan memb; 1.

R PRINS; PR00252; NRIONCHANNEL.

R PRINS; PR00252; NRIONCHANNEL.

R PROSITE; PS00236; NEUXORCHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1988; DB 5; Length 545;
Pred. No. 4.9e-165;
46; Mismatches 51; Indels 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.2%;
71.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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RA SEQUENCE FROM N.A.

RA SEQUENCE FROM N.A.

RA SCHULTE T., Oellers N., Adamczewski M.;

Rutarive alpha subunits of insect nicotinic acetylcholine receptors

RT "Putarive alpha subunits of insect nicotinic acetylcholine receptor alpha subunits.";

RT more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than

RT to other insect nicotinic acetylcholine receptor alpha subunits.";

RI SUBMILTARITY BELONGS TO THE EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

DR GO; GO:0005230; F: extracellular ligand-gated ion channel acti. . .; IEA.

GO; GO:0005230; F: extracellular ligand-gated ion channel acti. . .; IEA.

DR GO; GO:0005230; F: neurotransmitter receptor activity; IEA.

CO; GO:0005231; P: ion transport; IEA.

DR GO; GO:0005268; P: synaptic transmission; IEA.

DR GO; GO:0005268; P: synaptic transmission; IEA.

DR GO; GO:0005268; Neur channel LBD.

InterPro; IPR006029; Neur channel memb.

DR Pfam; PF02932; Neur chan LBD.

DR Pfam; PF02932; Neur channel memb; 1.

PR Pfam; PF02932; Neur channel memb; 1.

PR Pfam; PF02932; Neur channel memb; 1.
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                                                                                                                                                                                                  422 RCASATLPHQPTYYRTMYRQGDDGSVGPVGPAGPVVDGRLHEAIS-HTCLTSSAEYELAL
                                                                                                                                                        710 ILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV
556 MTPGGTLPHNPAFYRTVYGQGDDGSIGPIGST-----RMPDAVTHHTCIKSSTEYELGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Noctuoidea,
Noctuidae, Heliothinae, Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 LLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIIDVDEK
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PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last amorcation update)
Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
Heliothis virescens (Noctuid moth) (Owlet moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 496;
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68

308

249 VLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAESMPTTSDAVPLIGTYFNCIM

VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL

613 359 699 398

------MIRIVFLCWLPWILRMSRPGRPLILEFPTTPC

248 581

TYQINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQD 470

129 TYHTNIVVKHGGSCLYVPPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLNS **ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPC**

471 189 531

69 VDEKNOLLITULMLSLEMNDYNLRRNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG

VDEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLR I PPHR I WKPDVLMYNSADEGFDG

351

411

10 SLFVLLIFLAIIKESC-QGPHEKRLIAHLLSTYNTLERPVANESEPLEVKFGLTLQQIID

728

169

DIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHIIV

RTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILKEIRFITDQLRKDDECN

----TRKTILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI----

SDISSERKHQILS----DVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFY

614

360

670 399 729 453

582

309 FMVASSVVLTVVVLNYHHRTADIHEMPPWİKSVFLQWLPWİLRMGRPGRKI

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CHARLES TOUR THE LIGAND-GATEN (BY SIMILARITY).

CHARLES TOUR THE LIGAND-GATEN CONTROLL FAMILY.

BENEL, AFF21446, AAM1393-11,

BENEL, AFF21466, AAM1393-11,

BENEL, AFF21466, AAM1393-11,

BENEL, AFF21466, AAM1393-11,

BENEL, AFF21466, AAM1393-11,

BENEL, AFF21466, AAM1393-11,

BENEL, AFF21466, AAM1393-11,

BENEL, AFF21466, AAM1393-11,

BENEL, AFF21466, AAM1393-11,

BENEL, AFF2146, Find channel activity; IEA.

GO, GO:0005216; Find channel activity; IEA.

GO, GO:0005216; Find channel activity; IEA.

GO, GO:0005216; Find channel activity; IEA.

BENEL, AFF21466, BENEL, AAM1616, AAM1616,

BENEL, AFF2146, BENEL, AAM1616,

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DISSFVTNGEWELIGVPGKRNEIYYNCCPEPYIDITFAVVIRRKTLYYFFNLIVPCVLIA
                                                                                                                                                                                                                                                                                                                                                                                                    -----LAAHSCF--GVDYELSLILKEIRVITDQMRKDDEDADISRDW
                                                                               ---WIRIVFLCWLPWILRMSRPG---RPLILEFPTTPCS
                                                                                                                                                                                                                                                  DISSERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYG
                                                                                                                                                                                                                                                                                                                                                       QGDDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKDDECNDIANDW
                                                                                                                                                                                                317 SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLPWVLRMSRPGSATTPPPPARVPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21969411; PubMed=11973307; Grauso M.; Reenan R.A.; Chietto E., Sattelle D.B.; Grauso M.; Reenan R.A.; Chietto E., Sattelle D.B.; Movel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing."; Genetics 160:1519-1533(2002).
                                                                                                                                                                                                                                                                                                     -------DLELRERSSKSLLANVLDIDDDFRH-----PQAQQPQCCRYYR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotinic acetylcholine receptor Dalpha6 subunit variant type II.
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                               SMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 AA; 56048 MW; 6EE711810EDE7BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1625.5; DB 5; Pred. No. 2.3e-133; 47; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KFAAMVVDRLCLIFTMFAILATIAVLLSAPHIIVS
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61.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                    413 GGEENGAG-
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MEDLINE=19694011; PubMed=11973307;

Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,

Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a

New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-

Mediated A-to-I Pre-mRNA Editing.",

Genetics 160:1519-1533(2002).

-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-: SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ion channel acti.
                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last amotation update)
Nicotinic accetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF321445; AAM13392.1; ...
FlyBase; FBGN002151; nACR-alpha-30D.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel a
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0007268; P:synaptic transmission; IEA.
                                      494 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006201; Neur_channel.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006202; Neur_channel_memb.
Pfam; PF02931; Neur_chan_LBD; 1.
                                      PRT;
                                      PRELIMINARY;
                                      OBT7S3
œ
RESULT
                    Q8T7S3
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SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID 350

Gaps

79;

75; Indels

320; Conservative

Matches

291

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Similarity

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7

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Signal; Receptor SIGNAL 1
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01-JUN-2003
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                                                                                                                                                       SLFVLLFLAIIKESC-QGPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
                                                                                                                                                                                               69 VDEKNQILITINAWINLEWNDYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                       249 VLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIM
                                                                                                                                       291 SWIFLLIYLNASAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLOLSFGLTLMOIID
                                                                                                                                                                                    VDEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
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                                                                                                                                                                                                                                                                                                                                                                    ----WIRIVFLCWLPWILRMSRPGRPLILEFPTTPC
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                                                                                                                    Gaps
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Millar N.S.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ554(209; CAD86935.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005599; F:extracellular ligand-gated ion channel acti...
GO; GO:0005594; F:neurotransmitter receptor activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
InterPro; IPR006201; Neur_channel.
                                                                                                                  79;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                              Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                         309 FMVASSVVLTVVVLNYHHRTADIHEMPPWIKSVFLOWLPWILRMGRPGRKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nicotinic acetylcholine receptor subunit Dalpha6 precursor.
NACRALPHA-30D.
                                                                                             Length
                                                                                                                  77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             ----TRKIILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   729 DIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
                                                                     494 AA; 56095 MW; B46EBEDA63A92942 CRC64;
                                                                                            DB 5;
                                                                                          ; Score 1622.5; DB 5, Pred. No. 4.1e-133; 46; Mismatches 77;
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NBUROTR_ION_CHANNEL; 1.
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                                                                                           40.1%;
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                                                          Transmembrane
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NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                            19;
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Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Meoptera, Endopterygota; Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 FMVASSVVLTVVVLNYHHRTADIHEMPPWİKSVFLOWLPWİLRMGRPGRKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     729 DIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                        4DFC572139587070 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                40.1%; Score 1621.5; DB 5; 61.4%; Pred. No. 5.1e-133;
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InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006029; Neur chan LBD.
Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIOWCHANDEL.
IIGRAMS; IIGR0860; LIC; 1.
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                                                                                                                                                                                                                                                                                        55980 MW;
                                                                                                                                                                                                                                                                                                                                                                                         Matches 320; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 SDTSSERKHQILS----DVELKERSSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFY
            Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Balting."; Genetics 160:1519-1533 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 FMVASSVVLTVVVLNYHHRTADIHEMPPWİKSVFLQWLPWİLRMGRPGRKI-----
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                              -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
EMBL; AF321447; AAM13394.1; -.
                                                                                                K EMBLIA AFASTA47; ARMILSS94.1;
K EMBLIA AFASTA47; ARMILSS94.1;
K GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0005230; F:extracellular ligand-gated ion channel acti...;
GO; GO:0005216; F:ion channel activity; IEA.

GO; GO:0005216; F:ion channel activity; IEA.

R GO; GO:0005694; F:neurotransmitter receptor activity; IEA.

GO; GO:0006811; P:ion transport; IEA.

R GO; GO:0007268; P:synaptic transmission; IEA.

InterPro; IPR006202; Neur_channel.

R InterPro; IPR006202; Neur_channel.memb.

R Pfam; PF02291; Neur_chan_LBD; 1.

R Pfam; PF02291; Neur_chan_LBD; 1.

R PFTNTS; PR00252; NRIONCHĀNNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL----
                                                                                                                                                                                                                                                                                                                                                                                      79;
"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
                                                                                                                                                                                                                                                                                                                                                            5; Length 494;
                                                                                                                                                                                                                                                                                                        Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                      75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TRKTILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELIGDWKFAAMVVDRFCLIVFTLFTIIATVTVLLSAPHIIV 493
                                                                                                                                                                                                                                                                                                                                 494 AA; 56113 MW; 48327537229573FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.2e-133; ); Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 AA.
                                                                                                                                                                                                                                                                                                                                                           40.1%; Score 1620.5;
                                                                                                                                                                                                                                                                                          PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 61.0%;
Matches 318; Conservative 4
                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0860; LIC; 1
                                                                                                                                                                                                                                                                                                                    Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                              291
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01-JUN-2002 (TrEMBLrel. 21, Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 TVFLNLVAETLPQVSDAIPLLGTYFNCIMFMVASSVVLTVVVLNYHHRTADIHEMPPWIK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 NVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAV-THHTCI 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 TYHTNIVVKHNGSCLXVPPGIFKSTCKMDITWFPFDDQHCEMKFGSWTYDGNQLDLVLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDEKNOILTTINAMINLEWNDYNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                               SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLFVLLIFLAIIKESC-QGPHEKRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRTLYYFFNLIIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDGGDLSDF1TNGEWYLLAMPGKKNTIVYACCPEPYVDITFTIQIRRRTLYYFFNLIVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVFLCWLPWILRMSRPGRPLILEFPTTPCSDTSSERKHQILS----DVELKERSSKSLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TRKTILLSNRMKELELKERSSKSLLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0005230; F:extracellular ligand-gated ion channel acti.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:000594; F:ion channel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0007811; P:ion transport; IEA.
InterPro; IPR006201; Neur channel.
InterPro; IPR006202; Neur channel.
InterPro; IPR006202; Neur channel.
Ffam; PF02931; Neur channell.
Pfam; PF02931; Neur channell.
Pfam; PF02931; Neur channell.
01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Artropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLIASMALLGFTLPPDSGEKLSLGVTILLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1C200AF74F87F841 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 4.6e-132; 46; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch
39.8%; Score 1611;
al Similarity 58.2%; Pred. No. 4.4
320; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVFLOWLPWILRMGRPGRKI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59110 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                523 AA;
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617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=21966411; PubMed=11973307;

Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;

Mrovel Putrative Nicotinic Acetylcholine Receptor Subunit Genes,

"Novel Putrative Nicotinic Acetylcholine Receptor Subunit Genes,

"Tolphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a

"Tolphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a

"Tolphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify a

"Tolphas, Dalphas and Palpha7, in Drosophila melanogaster Identify a

"Tolphas, Dalphas, Dalphas, In Pre-mRNA Editing.";

"Genetics 160:1519-1533 (2002).

"I SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

"EMBL, AR31448, ARM133951.1, -..

"SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

"SPENSA, PERMO32151; nAcR-alpha-30D.

"GO; GO:0016021; C:integral to membrane; IEA.

"GO; GO:0016021; C:integral to membrane; IEA.

"GO; GO:0016021; F:ion tennel activity; IEA.

"GO; GO:00103249; F:neurocransmitter receptor activity; IEA.

"GO; GO:0012489; P:synaptic transmission; IEA.

"TH-ACPADATE TORONGOON."
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                                                                                                        SSVVLTVVVLNYHHRTADIHEMPQWIKSVFLQWLPWILRMSRPGKKITRK---TIMMNTR
                                                                                  -WIRIVFLCWLPWILRMSRPGRPLILEFPTTPCSDTS
                                                                                                                                                         SERKHQILSDVELKERSSKSLLANVLDIDDDFRHNCRPMTPG----GTLPHNPAFYRTV
                                                                                                                                                                                                                                  YGQG-----DDGSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDQLRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLFVLLIFLAIIKESC-QGPHEKRLINHLLSTYNTLERPVANESEPLEVKFGLTLQQIID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Nicotinic acetylcholine receptor Dalpha6 subunit variant type
NACR-ALPHA-30D OR NACR-BRA-30D OR BCDNA:GH01410 OR CG4128.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 509;
                                                                                                                                                                                                                                                                                                                                  DEBAELISDWKFAAMVVDRFCLFVFILFTIIATVAVLLSAPHIIV 500
                                                                                                                                                                                                                                                                                                           DECNDIANDWKFAAMVVDRLCLIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
       SMALLGFTLPPDSGEKLSLGVT1LLSLTVFLNMVAETMPATSDAVPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57887 MW; BE8D8E0198E0C2BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.6%; Score 1602; DB 5;
59.3%; Pred. No. 2.7e-131;
ive 48; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                               509 AA
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InterPro; IPR06202; Neur chan LBD.
InterPro; IPR066209; Neu channel memb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Pfam; PF02932; Neur_chan_memb; 1.-
PRINTS; PR00252; NRIONCHÂNNEL.
TIGRPAMS; TIGR00860; LIC; 1.
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PROSITE; PS00236; NEUROTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 59.3
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 AA;
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       535
                                                                                  582
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 KSSTEYELGLILKEIRFITDQLRKDDECNDIANDWKFAAMVVDRLCLIIFTMFAILATIA 759
                                                                            414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVVVRSGSSCLYVPPGIFKSTCKMDIAWFPFDDQHCDMKFGSWTYDGNQLDLVLKDEAGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schulte T., Oellers N., Adamczewski M.;

"Putative alpha subunits of insect nicotinic acetylcholine receptors

"Putative alpha subunits of insect nicotinic acetylcholine receptors

more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than

to other insect nicotinic acetylcholine receptor alpha subunits.";

L. Submitted (APR-1999) to the EMBL/Genbank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

R EMBL, AR143847; AAD32698.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005216; F:ion channel activity; IEA.

GO; GO:0005819; P:ion transport; IEA.

GO; GO:0007268; P:syraptic transmission; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · · ; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIIIRRRTLYYFFNLIIPCVLIA
                                                                                                                                                                                                                                                                                                                                                                                Heliothis virescens (Noctuid moth) (Owlet moth).
Bukaryota, Matazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota, Lepidoptera; Glossata; Ditrysia, Noctuoidea;
Noctuidae, Heliothine; Heliothis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQLDLQLQDETGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501;
                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative nicotinic acetylcholine receptor alpha 7-2 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501 AA; 56704 MW; 43CB0DC3960C78AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.8%; Score 1609; DB 5; 60.8%; Pred. No. 6.4e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
                                                                                                                                                                                                                                                                     501
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InterPro; IPR006202; Neur chan LBD.
InterPro; IPR00629; Neu chan LBD.
Pfam; PF02931; Neur chan LBD; 1.
Pfam; PF02932; Neur chan memb; 1.
PRINTS; PR00252; NRIONCHĀNNEL.
                                                                                                                                                                                                                                                                   PRT;
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VLLSAPHIIV
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Best Local Similarity
Matches 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane
                                                         200
                                                                                              454
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                                                                                                                                                                                                        RRKILYYFFNLIIPCVLIASMALLGFTLPPDSGEKLSLGVIILLSLTVFLNMVAETMPAT
                                                                                                                                                                                                                          249 RRRILYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLKLVAETLPQV
                                                                                                                                                                                                                                                                                                                                                        ---TRKTILLSNRMKELELKERSSKSLLANVLDIDDDFRHTI
                -DEKNOLLVTNVWLKLEWNDMNLRWNTSDYGGVKDLRIPPHRIWK
                               69 VDEKNQILTTNAMINLDEKNQLLITNIMLSLEWNDYNLRWNETEYGGVKDLRITPNKLWK
                                                                                              309 SDAIPLLGTYFNCIMFMVASSVVLTVVVLNXHHRTADIHEMPPWIKSVFLOWLPWILRMG
                                                                             PDVLMYNSADEGFDGTYQINVVVRNNGSCLYVPPGIFKSTCKIDITWFPFDDQRCEMKFG
                                                                                                                                           SWTYDGFQLDLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYIDITFAIII
                                                                                                                                                              ----WIRIVFLCWLPWILRMS
                                                                                                                                                                                                                                                                                                                                                                                                      655 PWTPGGTLPHNPAFYRTVYGQGDDGSIGPIGSTRMPDAV-THHTCIKSSTEYELGLILKE
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SGSQTAIGSSASFGRPTTVEEHHTAI-GCNHKDLHLILKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     714 IRFITDQLRKDDECNDİANDWKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHIIV 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ceinker S.E., Agbayani A., Arcaina T.T., Baxter B., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M. Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A., Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B., Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A., Zieran L.L., Rubin G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
NACR-ALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR CG4498 OR CG16878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR CG32975.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sethi H., Snir B., Svirskas R.R., Wan K.H., Weinburg T., Zieran L.L., Rubin G.M.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley; MEDLINE=99403001; PubMed=10471707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                       SDAVPL ----
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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
A Adams M.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.E.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani, A.A. A. H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Beasley E.M.,
Beson K.Y., Bencos P.W., Berman B.P., Bhandari D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Down D.E., Downes M., Dugan-Rocha S., Pleischmann W.,
A Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
Clodek A., Gong F., Garg N.S., Gelbart W.M., Glasser K.,
Alarris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alali M., Kalush F., Karpen G.H., We Z., Kennison J.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRHNQQLTTLQPRSLSTKH
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKNAQLKITEVDDDELWLAVRLAHCSSNISSSSTRTTSSNKRHNQQLTILQPRSLSTKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 HSNIASEQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSSNMLSPKTAAAATAAGDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTQQPTNIRLCARKRQRLRRRKRKRKPATPNETDIKKQQQLSMPPFKTRKSTDTYSTPAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLHVLQVLLVSLQQWQLHVQQRSVL
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                                                                                                                                                                                                                                                                                    Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                       5; Length 391;
                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                  E2AB465CF275E8C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
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                                                                                                                                                                                          Score 1502; DB 5,
Pred. No. 1e-122;
5; Mismatches 11
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PlyBase, FEGUNO28875; nAcR-alpha-34E. Hypothetical protein. SEQUENCE 391 AA; 43974 MW: F: PARAE!
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MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 NLSAKGECHLNYLECCMOH 319
                                                                                                                                                                                          Query Match 37.2%;
Best Local Similarity 94.4%;
Matches 301; Conservative
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Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., A Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy L., Muzhy D.M., Nelson D.L., A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Wenter E., Wang A.H., Wang X., A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., We J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zheng L., A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
I. The genome sequence of Drosophila melanogaster.";
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Baron J., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Baron J., An H., Baldwin D., Baranon G.C., Rogers Y.,

Barzon J., An H., Baldwin D., Baranon J., Beeson K.T., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

A Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Gonzalez M., Houck J. Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,

Rapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.

Matthews B.B., Bayraktaroglu L., Campbell K.,

Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

Clamp M., Drysdale R., Emmert D., Richter J., Russo S.,

Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,

Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E.,

Ashburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,

"Annotation of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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PRINTS; PR00252; NRIONCHANNEL.
TIGRFAMS; TIGROBGG; LIC; 1.
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Search completed: May 7, 2004, 11:38:36 Job time : 52.3701 secs

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Gaps

Best Local Similarity 47.99 Matches 286; Conservative

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291 SWIFLLIYLNLSAKVCLAGYHEKRLLHDLLDPYNTLERPVLNESDPLQLSFGLTLMQIID 350
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- nucleic search, using frame_plus_p2n modei OM protein

8, 2004, 11:50:34 ; Search time 5376.49 Seconds (without alignments) 4276.744 Million cell updates/sec May Run on:

US-09-303-232-2

1 MKNAQLKLTEVDDDELWLAV......MFAILATIAVLLSAPHIIVS 770 score: Scoring table: Sequence: Perfect

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62

27513289 seqs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

length: 2000000000 Minimum DB seq length: 0 Maximum DB seq length: 20 Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

EST 23-APR-2001

BG632919

GH16126.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128 'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence. BG632919.1 GI:13758409 EST. BG632919 RESULT 1 BG632919/c LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

Drosophila melanogaster (fruit fly) Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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GlyGluTrpGluLeuLeuGlyValProGlyLysArgAsnGluIleTyrTyrAsnCysCys
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/mol_yrpe="mRNA"
/db xref="taxon:727"
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/note="lorgan: head; Vector: pOT2; Site 1: ECORI; Site 2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
                                                                                                                                                                                                         Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798

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Indels:
         Ephydroidea; Drosophilidae; Drosophila
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Matches:
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                                                                                                                           Unpublished (2001)
Other ESTs: GH16126.5prime
Contact: Stapleton, M.
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9
                                                                                                     TITLE
JOURNAL
COMMENT
                                      REFERENCE
AUTHORS
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
Was normalized. Library was constructed by Life Technologies, a
division of Invitogen. This sequence belongs to sequence cluster
7646.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=Cs0D007CH03QPl&cluster=7646.r. Contact :
Feng liang Bmail : fliang@lifetech.com URL :
Feng liang Bmail : fliang@lifetech.com URL :
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD007CH03QPl.
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                                                                                                                                                       346
                    406
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/clone lib="NGUNOBLASTOMA COT 50-NORMALIZED"
/clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12793792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 ValpheLeuAsnMetValAlaGluThrMetProAlaThrSerAspAlaValProLeu 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 GTCTTCCTCAACAGTGGCGGCGAACAATGCCGGCGGCGACCTCCGATGCGGTACCGCTG 169
                                                                                                                            PhePheAsnLeullelleProCysValLeulleAlaSerMetAlaLeuLeuGlyPheThr
                                                                                                                                                                                                                                                           LeuProProAspSerGlyGluLysLeuSerLeuGlyValThrIleLeuLeuSerLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                285 craccaccacarreregramanacerregeringanarrerarrerarrared
GGCGAATGGGACTTGTTAGGTGTGCCCGGTAAACGAAATGAAATCTACTATAATTGCTGC
                                                                                             ProGluProTyrIleAspileThrPheAlaileIleIleArgArgArgThrLeuTyrTyr
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Tumor Gene Index

In Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANL228 row: f column: 14
High quality sequence stop: 746.
                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"

db xref="taxon:8155"

clone="IMAGE:6642638"

/tissue_type="cocytes"

/lab_host="DHIOB (phage-resistant)"

/clone=lib="NICHD XGC_OOI"

/note="Workor: pCMV-SPORT6; Site 1: Not1; Site 2: Sal1;

cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Life Technologies."
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       1 (bases 1 to 922)
NCI--CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 ArgileTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 CAGATTTGGAAGCCTGATATTCTTCTTCTATAACAGTGCAGATGATAGATTTGATGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 TyrGlnThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProProGly1le
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AUTHORS
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                                GCAAGCGAGTWCCAGAGGAAGCTTTACAAGGAGCTGGTCAAGAACTACAATCCCTTGGAG 246
                                                                     ArgProValLeuAsnGluSerAspProLeuGlnLeuSerPheGlyLeuThrLeuMetGln 347
                                                                                            IlelleAspValAspGluLysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGlu 367
                                                                                                                                                                     388 IleProProHisArgileTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGly 407
                                                                                                                                                                                                                                                                                                                                                                 PheAspGlyThrTyrGlnThrAsnValValValArgAsnAsnGlySerCysLeuTyrVal 427
                                                                                                                                                                                                                                                                                                                                                                                        ProProGlyIlePheLysSerThrCysLysIleAspIleThrTrpPheProPheAspAsp 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuGlnAspGluThrGlyGlyAspileSerSerTyrValLeuAsnGlyGluTrpGluLeu 487
AlaGlyTyrHisGluLysArgLeuLeuHisAspLeuLeuAspProTyrAsnThrLeuGlu 327
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ATGCAGGAG------GCAGATATCAGTGGTATATCCCCAATGGAGAATGGGACCTA 717
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Edenopus laevis
Edenopus netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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US-09-303-232-2 (1-770) x AY402873 (1-1436)	312			Oy 352 AspGluLysAsnGlnLeuLeuValThrAsnValTrpLeuLysLeuGlufTrpAsnAspMet 371	372	201 AACTGAAGTGGAACCCCTCTGACTATGGTGGGGCAGAGTTCATGCTGGTGCGCACAG	Cy 392 ArgileTrpLysProAspValLeuMetTyrAsnSerAlaAspGluGlyPheAspGlyThr 411	201 MAGNITICIUGGAGUUGGAGUTIGIGCIGIATAACAATGCTGTTGGGGGATTTCCAGGTGGAC 412 TVTGINTHTAGNVAIVAIVAIAAAAAAAAAAAAAAAAAAAAAAAAAAAA			Db 381 TTTAAGAGCTCCTGTAAAATCGACGTGACCTACTTCCCGTTTGATTACCAAAACTGTACC 440	Qy 452 MethysPhedlySerTrpThrTyraspdlyPhedlnLeuaspLeuGlnLeuglnaspdlu 471		Db 498 TCTTCCATGAACCTCAAGGACTATTGGGAGGGGGGGGGG	Oy 492 GlyLysArgAsnGlulleTyrTyrAsnCysCysProGluProTyrIleAsplleThrPhe 511	512 Alaileileileardardardardhrionthrachababbaban an i ail an an an an an an an an an an an an an		Db 678 CTCATCTCCTCACTGTGCTCGTCTTCTACCTGCCCTCCGGCTGGGGAGGTG 737	Qy 552 SerleuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAlaGluThr 571 :::	738	Qy 572 MetProAlaThrSerAspAlaValProLeu	86/ 1		8 2 3		918	595 LeuArgMetSerArgProGlyArgProLeuIleLeuGl	978	VY 615 ASPThrSerSerGluargLysHisGlnIleLeuSerAspValGluLeuLysGluArgSer 634 ::: ::	
649	DD 1436 GACAGATGGGCATGTGCAGGTCATGTGGCCCCCTCTGTGGGGCACCCTC1483 Qy 667 AlapheTyrArgThrValTyrGlyGlyGlyGlyAsnasnasnalycertlaclynaning	1484	687 ThrArgMetProAspAlaValThrHisHisThrCysIleLysSerSerThr	Db 1532 GCTCTGCTGCAGGAGGCTGCTGCTGTTATCACCCCAC			DD 1622 GAGGALGCTGGACTCTTCGGTGAAGAGGACTGGAAGTATGTTGCCATGGTCATGGACAGG 1681 QY 744 LeuCysLeullellePheThrMetPheAlaileLeuAlaThrTlealaYaltanton 763	Db 1682 ATCTTCCTCTGGCTGTTTATCATCGTCTGCTTCCTGGGGACCATCGGCCTCTTTCTG 1738	T 5 873	LOCUS AY402873 1436 bp DNA linear GSS 15-DEC-2003 DEFINITION Homo sapiens CHRNA3 gene, VIRTUAL TRANSCRIPT, partial sequence,	ACCESSION AY402873 VERSTON AVA02872 CT. 2017001	S	-	KEFEKENCE I (bases 1 to 1436) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., M Ferris, S., Wang, G., Zheng, X.H., White, T.J., Sni Adams, M.D. and Cargill, M.	111LE Interring nonneutral evolution from human-chimp-mouse orthologous gene trios	AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,W.	Ą.	COMMENT This sequence sequencing genomic exons and ordering them based on alianment	FEATURES Location/Qualifiers source 11436	/organism="Homo sapiens" /mol type="genomic DNA"	/db_xref="taxon:9606" gene <1>1436	/gene="CHRNA3" /locus tag="HCM1369"	ORIGIN	T. British .	837.50 milarity: 54.71%	: 35.25% Mismatches: 20.71% Indele	Gaps:	

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Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKO53497
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:El30103El4 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
                                                                                                                                                                                                                                                                                                                    1215 TCC------CICTCTGCTTTGTCACCAGAATCAAAGCCATCCAAAGTGTC 1262
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                      635 SerLysSerLeuLeuAlaAsnValLeuAspIleAspAspAspPheArgHisAsnCysArg 654
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 tull-length cDNAs

Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayasu, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Konda, M., Kagwai, T., Kasula, M., Kaya, S., Kurihara, C., Matsuyama, T., Kanoh, H., Kawai, J., Kasikawa, T., Katoh, H., Kawai, J., Konda, M., Ohasto, N., Ohasaki, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, J., Saito, R., Sakai, C., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, M., Tagawa, A., Takabashi, F., Takaku, Akahira, S., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai
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PFDYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHEIKXNCC
EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYLFSDCGEKVTLCISVLLS
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WVRAVFLNILDRYMFMTRPTSTEEDAPKTRNFYGAELSNLNCFSRADSKSCKEGYPCQ
DGTCGYCHHRRVKISNFSANLTRSSSSESVDAVLSLSALSPEIKEAIQSVKYIAENMK
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RPVANVSHPVIIQFEVSMSQLVKVDBVNQIMETNLWLKQIWNDYKLKWKRSDYQGVEF
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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="0 day neonate"
94. [1593
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URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"

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/strain="C57BL/6J"
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Pred. No.:
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<u>.</u>

Db 1084 ACGATGCCACTTGGGTCAAGGCTGTGTTTTTGAACCTTCTCCCCAGGGTG Qy 598 SerArgProLeuIleLeuGluDheProThrThrProCysSerA Db 1144 ACTAGGTCA	618	Qy 638 LeuLeuAlaAsnValLeuAspIleAspAspAspPheArgHisAsnCySArgP 	Qy 658 ProGlyGlyThrLeuProHisAsnProAlaPheTyrArgThrValT	Qy 676 GlyAspAspGlySerIleGlyProIleGlySerThrArgMetProAspAlaV	Qy 696 HisThrCyslleLysSerSerThrGluTyrGluLeuGlyLeuIleLeuLysG	Oy 716 PhelleThrAspGlnLeuArgLysAspAspGluCysAsnAspIleAlaAsnA	Oy 736 PhealaAlaMetValValAspArgLeuCysLeuIleIlePheThrMetPheA :::	Qy 756 AlaThrIleAlaValLeuLeu 762 	RESULT 7 AKO51730 LOCUS AKO51730 AKO51730 AKO51730 BEPINITION Mus musculus 12 days embryo sminal gandion onto premi		S HTC; CAP trapper. Mus musculus (house mouse) ISM Mus musculus (house mouse) Filerrorta: Matazza: Choodata	Rodentia; Sciashizaki, Y.		AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shiba Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashi TILE Normalization and subtraction of cap-trapper-selected or prepare full langer forms live in the selected or prepare full langer forms live in the selected or prepare full langer forms live in the selected or se	AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H. Sumi, N., Ishi, Y., Nakamas, G., Ustan, M., William, M., W	Yamamoto, P. Matsumoto, P. Sakaguchi, S. Hegami, T. Ka Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohaza, E., W Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S
: 826.50 nt Similarity: 54.04% Local Similarity: 34.71% Match: 11.44%	OS-03-503-232-2 (1-770) x AKO53497 (1-1864) QY 295 LeubeulleTyrLeuAsnLeuSerAlaLysValCysLeuAlaGlyTyrHisGluLysArg 314	LeuleuHisAspLeuleuAspProTyrAsnThrLeuGluArgProValLeuAsnGluSer 33:				PheAspGlyThrTyrGlnThr 41	ProProGlyllePheLysSer 4	31nArgCysGluMetLysPhe 	.euGlnAspGluThrGlyGly TCATTGGCTCCTCCATG	Oy 475 AspileSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyValProGlyLysArg 494			1yGluLysLeuSerLeuGly ::::: GGGAGAAGGTGACGCTCTGC		581	UD 1024 TIGICCATCGTCATCACAGTCTTIGIGCTCAACGTGCACTACAGAACTCCGACCACACAC 1083 Qy 582TrplleArglleValPheLeuCysTrpLeuProTrplleLeuArgMet 597

snasptrplys 735 ::||||||||| argarregaag 1482 HTC 20-SEP-2003 IKEN full-length NICOTINIC Sequence. nibata,K., Ishizaki,Y. ed cDNAs to :ry of new genes ----ACCAGC 1158 Sasaki,N., Carninci,P.,
Tashiro,H., Itoh,M.,
Nishine,T., Harada,A.,
egami,T., Kashiwaqi,K.,
Ohara,E., Watahiki,M., CTACGGTGCT 1200 GGAAGGCTAC 1260 AAAAATCTCA 1314 ||||| | TGTGTTGTCC 1374 : ::::: AAGTGTGAAG 1422 rAspThrSer 617 ||||||| GTGCATTTTA 1542 rSerLysSer 637 gProMetThr 657 TyrGlyGln 675 aValThrHis 695 sGlulleArg 715 eAlaileLeu 755 Euteleostomi; Murinae; Mus.

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980 ATCTCCGTGCTCCTCTCCTGACGGTCTTTCTCCTCGTGATCACGGAGACCATCCCTTTC 1039
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AQNYAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFLQPLMARDDT"
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Query Match:
                                                            polyA_signal
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                                                                                                                   polyA_site
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/dev stage="12 days embryo"
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                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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           Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159 3 5hibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakajuchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., KIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 531-573 (2002) 6 (bases I to 3126) Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Haragaka,T., Haraoka,T., Hiraoka,T., Haysshida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hiraoka,T., Hayshida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Kouda,M., Katchi,H., Kawal,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Kya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,A., Murata,M., Okazaki,Y., Salto,R., Saltoh,H., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Takaku-Akahira,S., Sogabe,Y., Tagami,M., Tagawa,A., Takaku-Akahira,S.,	Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216) Fax:81-45-503-9216) Fax:81-45-503-9216 Genomic Science and Sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to Please visit our web site for further details.	URL:http://ganome.gsc.riken.go.jp/ URL:http://ganome.gsc.riken.go.jp/ Location/Qualifiers 113126 113126 /organism="Mus musculus" wol_type="mRNA" strain="CSTBL/6J" db_xref="RANTOM_DB:A730007P14" db_xref="RANTOM_DB:A730007P14" db_xref="RANTOM_DB:A730007P14" db_xref="RANTOM_DB:A730007P14" db_xref="Laxon:10090" clone="A730007P14" tissue type="cerebellum" clone lib="RIKEN full-length enriched mouse cDNA library" dev_ctage="7 days neonate" clone lib="RIKEN full-length enriched mouse cDNA library" dev_ctage="7 days neonate" clone lib="RIKEN full-length enriched mouse cDNA library" dev_ctage="7 days neonate" clone lib="RIKEN full-length enriched mouse cDNA library" dev_ctage="7 days neonate" looklength enriched mouse cDNA library" dev_dence: FASTY, 99.8%ID, 100%length, match=1497)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A..
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                                        Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                               Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M. A., Tanenbaum, D. M., Civello, D. R., Lu, F., Murphy, B., Ferriera, S., Wang G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, M. 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
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94
156
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Matches:
Conservative:
Mismatches:
Indels:
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1. .1436
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                                 1 (bases 1 to 1442)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
           Eukaryoca, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                        Direct Submission Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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LeuAspLeuGlnLeuGlnAspGluThrGlyGlyAspIleSerSerTyrValLeuAsnGly
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                                                                                                                                 GluProTyrIleAspIleThrPheAlaIleIleIleArgArgArgThrLeuTyrTyrPhe
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|-----cccgacagcagcccggccagccagccttcccg-----
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                                               PhelysSerThrCysLysIleAspIleThrTrpPheProPheAspAspGlnArgCysGlu
                                                                                                    TyrGlnThrAsnValValValArgAsnAsnGlySerCysLeuTyrValProProGly1le
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1 (Pases 1 to 1374).

Clark, A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
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Clark, A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Mang,G., Zheng,X.H., White,T.J., Shinsky,J.G.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/db_xref="taxon:9606"
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	Db 1200 AGGTCCTCTGGGAGGTTCCGGCAAGATCTACAGGAAGCATTAGAGGGCGTCAGCTTCATC 1259 Qy 718 ThrAspGlnLeuArgLysAspAspGluCysAsnAspIleAlaAsnAspTrpLysPheAla 737	Db 1260 GCACAGCATTTGGAGGAGTGATCGAGAGTGTCATCGAGGACTGGAATTCGTC 1319 Oy 738 AlaMetValValAspArgLeuCysLeuIlellePheThrMetPhealaileLeuAlaThr 757		SULT 13 6406232 AY406232 1374 bp DNA linear GSS 1 FINITION Wis mischillis Cubaxi GSS 1		OKCANISM Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. REFERENCE 1 (bases 1 to 1374) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Keiariwal a	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous	gene trios Science 302 (5652), 1960-1963 (2003) 14671302 2 (bases 1 to 1374)	AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.	JUTLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, ROCKVILLE, MD 20856, USA COMMENT This sequence was made by sequencing genomic exons and ordering	Them based on alignment. FEATURES Location/Qualifiers source 11374 /organism="Mus musculus"	/mol_type="genomic DNA" /db_xref="taxon:10090" <1	ORIGIN /locus_tag="HCM2488"	Alignment Scores: Pred. No.: 8.6e-61 Length: 1374 Score: 797.00 Matches: 169 Percent Similarity: 51.97\$ Conservative: 95 Best Local Similarity: 33.27\$ Mismatches: 140	19.71% Indels: 29 Gaps: 0) x avancos (1.737.1)	heleuleuile	

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L Nature 420, 563-573 (2002)

B (bases 1 to 429)

S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Haramoto, K., Hiraoka, T., Hirozane, T., Hori, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, Y., Miyazaki, A., Murata, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakaume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sakaume, N., Sogabo, Y., Tanaka, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takamatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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LLVIVBELPEYTSSAVPLIGKYMLFTWYFVIASIIITVYINNHHRKSPSTHIMPEWVRK
VFIDTIPNIMFESTMKRPSKDKQEKRIFTEDIDISDISGKPGPPPMGFHSPLIKHPEV
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/clone="4831406G09"
/clone lib="RIXEN full-length enriched mouse cDNA library"
/dev stage="0 day neonate"
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/translation="MELSTVLLLLGLCSAGLVLGSEHETRLVAKLFEDYSSVVRPVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, VRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                  Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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The FANTOM Consortium and the RIKEN Genome Exploration Research
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Matches:
Conservative:
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                ----CCACCTATG 1140
                                                                                                                                                                                                                                                                                                                                                                                             1141 GGCTTTCACTCTCCGCTGATCAAGCACCCT-----GAGGTGAAAAGCGCCATCGAG 1191
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1252 GAATGGAAGTATGTCCATGGTGATGGATCACATCCTCCTCGGAGTCTTATGCTGGTG 1311
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Wis musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4831406G09 product:cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle), full insert sequence.
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspTrpLysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrMetPhe
                                                                                                653 CysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyrArgThrVal
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         1066 AAACAAGAGAATTTTACAGAAGACATAGATATATCTGAC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Cy 593 Trp11eLeuArgMetSerArgProGlyArgProLeu11eLeuGluPheProThrThrPro 612	Cy 613 CysSerAspThrSerSerGluArgLysHisGlnIleLeuSerAspValGluLeuLysGlu 632 :::::: Db 1077TCCAGAGAT 1085	Qy 633 ArgSerSerLysSerLeuLeuAlaAsnValleuAsplleAspAspAspPheArgHisAsn 652 :::	Oy 653 CysArgProMetThrProGlyGlyThrLeuProHisAsnProAlaPheTyrArgThrVal 672 Db 1130 1130	Qy 673 TyrGlyGlnGlyAspAspGlySerIleGlyProlleGlySerThrArgMetDroAspAla 692 Db 1131ATCICTGGGAAGCCGGGTCCTCCACCTATG 1160	Qy 693 ValThrHisHisThrCysIleLysSerSerThrGluTyrGluLeuGlyLeuIleLeuLys 712	Qy 713 GluIleArgPheIleThrAspGlnLeuArgLysAspAspGluCysAsnAspIleAlaAsn 732	Qy 733 AspTrpLysPheAlaAlaMetValValAspArgLeuCysLeuIleIlePheThrMetPhe 752 ::: ::: ::: ::: ::: Db 1272 GAATGGAAGTATGTTGCCATGGTGATCACATCCTCCTCGGAGTCTTATGCTGGTG 1331	Qy 753 AlaileLeuAlaThrileAlaval 760 :::::: Db 1332 TGTCTCATCGGGACGCTGCCTGG 1355	RESULT 15 AV402877 LOCUS DEFINITION Pan troglodytes CHRNB4 gene, VIRTUM, TRANSCRIPT, nartial semiance	equence. 9758860	SM	REFERENCE 1 (bases 1 to 1442) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D. M., Civello, D.K., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zhang, X.H., White, T. I. Sninsky, T.		14671302 2 (bases 1 to 1442) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejari Todd, M.A., Tanenbaum, D.M., Civello, D.R., Iu. F., Murnhy	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,	Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and them based on alignment.	FEATURES Location/Qualifiers Source 11442 /organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598"
Best Local Similarity: 33.27% Mismatches: 140 Query Match: 19.71% Indels: 104 DB: 1 Gaps: 8 US-09-303-232-2 (1-770) x AX029177 (1-4290)	SerTrpllePheLeuLeulleTyr ::: TGACTGTTCTCCTGCTAGGG	COTYXASNIThrLeuGluArgProVal	leasp ::: Caar			AspGly 41	roGly 4 CAGCC 4	rgCys ACTGC	Qy 451 GluMetLysPheGlySerTrpThrTyrAspGlyPheGlnLeuAspLeuGlnLeuGlnAsp 470	Qy 471 GluThrGlyGlyAspileSerSerTyrValLeuAsnGlyGluTrpGluLeuLeuGlyVal 490 :::	Qy 491 ProglyLysArgAsnGlulleTyrTytAsnCysCysProGluProTyrIleAspIle 509	Oy 510 ThrPhealallellelleArgArgArgThrLeuTyrTyrPhePheAsnLeuIlellePro 529	Oy 530 CysValLeuileAlaSerMetAlaLeuLeuGlyPheThrLeuProAspSerGlyGlu 549	Oy 550 LysLeuSerLeuGlyValThrIleLeuLeuSerLeuThrValPheLeuAsnMetValAla 569	QY 570 GluThrMetProAlaThrSerAspAlaValProLeu 581 :: ::	Qy 581 581 Db 924 AIGGICTITGCATIGGGICCAICATCACGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	2

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Pred. No. is the number of results predicted by chance to have a

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ALIGNMENTS

		AF143846 3629 bp mRNA linear TNV 27-MAY-1999	Heliothis virescens putative nicotinic acetylcholine receptor alpha	7-1 subunit mRNA, complete cds.	AF143846	AF143846.1 GI:4895004		Heliothis virescens (tobacco budworm)	Heliothis virescens	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptervoota:	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;	Noctuoidea; Noctuidae; Heliothinae; Heliothis.	1 (bases 1 to 3629)	Schulte, T., Oellers, N. and Adamczewski, M.	
RESULT 1	AF143846	LOCUS	DEFINITION He	7	ACCESSION A	VERSION A	KEYWORDS .	SOURCE He	ORGANISM He	鱼	Ň	N	REFERENCE 1	AUTHORS Sc	

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DITWFPFDDQRCEMKFGSWTYDGYQLDLQLQDEGGGDISSFYTNGEWELIGVPEKRNE
    Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha
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100.0%; Pred. No. 7.2e-291;
ive 0; Mismatches 0; Indels 0;
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/product="putative nicotinic acetylcholine
7-1 subunit"
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                                                                                      Unpublished
2 (bases 1 to 3629)
Schulte,T., Oellers,N. and Adamczewski,M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG, 51368, Germany

    3629
    organism="Heliothis virescens"

                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:7102"
335, .1825
/note="hvnachra7-1"
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Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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THEMSDWIRCVFLYMLPWVLRMSRPGSATTPPPARVPPPPDLELRERSSKSLLANVLD
IDDDFRHPQAQQPQCRYYRGGEENGAGLAAHSCFGWDYELSLILKRITVJTDQMRKD
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                                                                  Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.
Nucleic acids encoding acetylcholin-receptor subunits from insects
Patent: EP 0962528-A 3 08-DEC-1999;
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                Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Noctuoidea, Noctuidae, Heliothinae, Heliothis.
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                                                                                                                                                    /organism="Heliothis virescens"
/mol_type="unassigned DNA"
/db_xref="taxon:7102"
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3701)

Martin,A., Nadja,E. and Thomas, Heliothis.

Datent: JP 2000023680-A 2 25-JAN-2000;

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O Heliothis virescens

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100.0%; Score 1488; DB 6;
Best Local Similarity 100.0%; Pred. No. 7.2e-291;
Matches 1488; Conservative 0; Mismatches 0;
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1, 3701
/ Organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="taxon:7102"
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Query Match Best Local Similarity 64.6%; Pred. No. 3.7e-114; Matches 950; Conservative 0; Mismatches 515; Indels 6; Gaps 2; 21 CTCGCACTTGGGGGCCGGGGCCTGCTGCTGCTGTGCTGT		GTACGTGCCGCCCGGCATCTTCAAGAGCACTTGTGGTCAAACATGGCGGCAGTTGTCT 80 GTACGTGCCGCCCGGCATCTTCAAGAGCACCTTGTGGTCAAACATGGCGGCAGTTGTCT 80 GTACGTGCCCCCCGGCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCTT 50 GTACGTGCCCCCCTGGTATCTTCAAGAGCACATGCAAGATCGACATCACGTGGTTCCCATT 86 CCAACGACCAACCAACGAAGAAATTCGGTAGTTGGACTTTATGATGGTTATCAGTTGGA 92 TCTACAACTACAAGAAATGAAATTCGGTAGTTTGTCACGAATGGCCAATGG 98 GGAGTTATTGAATTCCGAAGAGGGGGGGAATCTTTCCGATTTTATCACAATGGCGAATG 98 GGAGTTAATAGGATCCCCGGCAAGGGGGAATCTTTCCGATTTTATAAAATGCCGAGGC 68 GGAGTTAATAGGATCCCCGGCAAGGGGGAATCTACAACTTCTTCCCAAAATCCACTCGCCCAAAACCT 10	81 ATACATCGACATCACGTTTCGGTGGTGGAGAAAACGCTCTACTACTTCTTCCA 740 47 ATACATCGACATCACGTTTGCGTGGTGGAGAAAACGCTCTACTACTTCTTCCA 740 41 ATACATCGACATTTGCGTGGTGGTGTCGTCGCTCTATTATTTTTTCA 110 41 ATACTCGACATCTCTTACTATACAAATTCGTCGCTCTATTGGGGTTCACCTTGCCTC 800 07 TTTAATCGTGCCTGGTGGTGCTCATTGGGCTTCACATTGCCGCC 116 07 TTTAATCGTGCCTGGTGGTGTGTGTGATGGCCTACTGGGCTTCACATTGCCGCC 116 08 AGACTCCGGAGAAAATTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCT 860 07 GAATTCGGGCGAGAAACTGACGGCGTAACTAACTGACGTTATTCT 122	861 CAACATGGTGGCGGAGACGATGCCAGCGACGACGACCCTGCTTGCT
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	Jox, UK Location/Qualifiers 12023 (organism="Drosophila melanogaster" /mol_type="mRNA" /db_xref="taxon:7227" /dav_stage="embryo" 12023 /gene="nAcRalpha-30D" 3791863 /gene="nAcRalpha-30D" /note="nAcRalpha-30D" /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b and 8a"	/product=Inicotinic acetylcholine receptor Dalpha6 subunit variant type II" /product=Inid=AAM1339.1" /product=Inid=AAM1339.1" /db xref="GI:2015284" /db xref="GI:2015284" /translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLINHLLSTYNTL ERPVANESEPLEXKFCLTLQQIDVDEXMOLLITNIAMSLEWNDYNLEWNETFEGGVK DLRITPNKLMKPDVLMANADEGFDGTYHTNIVKGHGSCLYVPPGIFKSTCKDITW FPFDDQHCENKFGSWTYDGNQLDIVANSEDGGDLSDFTUNGENYLLAMFCKTNIVYA CCPEPYVDITFTIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTGVTIL LSLITVFLNIVNSENPTTROAPLINTREATILINE PPWIKSVFLOWLPFWIIRMGREGKTTRKTILINFRNELELKERSSKELLANVLDIDD DFRHTISGSGTAIGSSASFGRPTTVEEHHTALGCNHKCDLHLIKKELQFTTARNEKADD DFRHTISGSGTAIGSSASFGRPTTVEEHHTALGCNHKCDLHLIKKELQFTTARNEKADD 793. 794 /gene="results in glycine to asparagine substitution; compared to the sequence deposited in GenBank Accession Number zenonsc		1314 fane="nAcRalpha-30D" fote="compared to variant clone" replace="a" fene="nAcRalpha-30D" fote="compared to variant clone" replace="t" fene="nAcRalpha-30D" fote="compared to variant clone" fote="compared to variant clone" fote="nAcRalpha-30D" fote="compared to variant clone" replace="t"
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                                                                                                                                                                                                      Score 611.8; DB 3;
Pred. No. 1.6e-113;
); Mismatches 517;
                                                               'gene="nAcRalpha-30D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLMISLEMNDYNLEWNETEYGGYK
DLRITPNKLWREDVLMYNSADEGFDGTYHTSVVVKHGGSCLYVPPGIFKSTCKMDITW
FPFDQARCEMKFGSWTYDGNQLDLVLSSEDGGDLSDFTINGEWYLLEMPGKKWTIVYA
CCPEPTQTTQITRRDLYYFFNLLVPCVLISSMALLGFTLPPDSGEKTJTGYTLL
LSLTVPFNLLVAESEMPTEGAVPHOLIGYFPNCINFWVASSVVLTVVVLNYHHRTADIHEM
PPWIKSVFLQMLPWILRMGRPGRKITRKTILLSNRMKELELKERSSKSLLANVLDIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MDSPLPASLSLFVLLIFLAIIKESCQGPHEKRLLNHLLSTYNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology, University College London, Gower Street, London, WCIE 6BT, UNITED
CGCCATTGGCTCGTCGGCCAGCTTCGGTCGGCCCACACGGTGGAGGAGCATCACACGGC
                                                                                                  AATACTATTAAGCAATCGCATGAAGGAGCTGGAGCTAAAAGGAGCGCTCCTCCAAATCCCT
                                                                                                                                        CCTAGCGAACGTGCTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCAGCCGCA
                                                                                                                                                                                                                      ATGCTGCCGATACTACAGGGGGGGTGAGGAGAATGGCCGCGGGGTTGGCCGCGCGCACAGTTG
                                                                                                                                                                                                                                                                                                CTTCGGTGTCG---ACTACGAGCTCTCCCTCATTCTGAAGGAGATTAGAGTCATCACAGA
                                                                                                                                                                                                                                                                                                                                     CATCGGCTGCAATCACAAGATCTTCATCTAATTCTCAAAGAATTGCAATTTATTACGGC
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                                                             GGCGCGCGTA----CCTCCGCCGCCGGACCTGGAGCTGCGCGAGCGCTCCTAAGTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="nicotinic acetylcholine receptor subunit
Dalpha6"
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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nAcRalpha-30D gene; nicotinic acetylcholine receptor
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/db_xref="G1:29466435"
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/db_xref="taxon:7227"
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/gene="nAcRalpha-30D"
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Millar,N.S.
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AUTHORS
TITLE
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reflect accurately this particular CDNA clone. However, there are artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unsplaced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site changefruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGIFKSTCKMDITWFPFDDQHCBMKFGSWTYDGNQLDLVLSSEDGGDLSDFITNGEWY
LLAMPGKKNTIVYACCPEPYVDITFTIQIERRTLYYFFNLIVPCVLISSMALLGFTLP
PBGGSKLITGVTILLSLTVELNLVBESMFTTSDPVDLIGFYFNCIMFWVASSVVTTVV
VLNYHRTADIHEMPPWIKSVFLQMLPWILRMGRFGRKITRKTILLSNRWKELELKER
SSKSILANVLDIDDPFRHTIGGSQFAIGSSASFGRRPTVEEHHTALGCNHKDLHLILK
ELQFITARNMKADDEAELIGDWKFAAMVVDRFCLIVFTLFTILATVTVLLSAPHIIVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="PFNPRATRYKQAKDMDSPLPASLSLFVLL1FLAIIKESCQGPHB
KRLLNHLLSTYNTLERPVANESEPLEVKFGLTLQQIIDVDEKNQLLITNLWLSLEWND
YNLRWNETEYGGVKDLRITPNKLWKPDVLMYNSADEGFDGTYHTSVVVKFGGGSCLYVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCTGTCAAGGACCTCATGAAAAGCGCCTGCTGAACCATCTGCTGTCCACCTACAATAC
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Pred. No. 1.6e-113;
0; Mismatches 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="GH15518p"
/protein_id="AARR82B15.1"
/db_xref="G1:40216008"
/db_xref="FLYBASE:FBGN0032151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="nAcRalpha-30D"
'db_xref="FLYBASE:FBgn0032151"
                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="nAcRalpha-30D"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
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'codon_start=2
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                                              CTTCAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCACCATACTGATCCTCAA
                                                                                                                     CTACCACCACCGCCACGCACACTCACGAAATGAGTGATTGGATTCGTTGCGTGTTCCT
                                                                                                                                                                    CTACCACCATCGCACAGGGGACATTCACGAGATGCCACCGTGGATCAAGTCCGTTTTTCCT
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melazogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Lawrence Berkeley National Laboratory, One Cyclotron Road,
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1699)
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GH15518 full insert cDNA.
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laborat
Berkeley, CA 94720
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/ Franslation="MOSPLPASLSLPVLLIFLATIKESCQGPHEKRLLANHLLSTYNTL
ERPVANDSEEPLEWKFGLTLQQIIDVDEKNQLLITALMALSLEMNDYNLEWNETEYGGWY
DLRITDWKLWRPDVLMYNSDDGGFDGTYHTNIVVKRSGSCLYVPPGIFKSTCKNDITW
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DFRHTISGSQTAIGSSASFGRPTTVEEHHTAIGCNHKDLHLILKELQFITARMRKADD
                          INV 29-APR-2002
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1 (Bosses 1 to 2023)
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putarive Nicotinic Acetylcholine Receptor Subunit Genes, Naphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing
  Ar321447 29-APR-20 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type III (nAckalpha-30D) mRNA, complete cds, abstratively spliced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
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in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ion channel; neurotransmitter transmembrane receptor; alternatively spliced; contains exons 3b /codon_start=1
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llarity 64.4%; Pred. No. 1.6e-113;
Conservative 0; Mismatches 517;
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                                                                                                                                                                       Drosophila melanogaster (fruit fly)
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/protein_id="AAM13394.1"
/db_xref="GI:20152849"
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gene="nAcRalpha-30D"
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/db_xref="taxon:7227"
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/dev_stage="embryo"
1. .2023
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Grauso, M. and Sattelle, D.B.
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Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphae and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I PPE-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6 subunit variant type I (nAcRalpha-30D) mRNA, complete cds, alternatively spliced.
AF321445.1 GI:20152844
                   AATACTATTAAGCAATCGCATGAAGGAGCTGGAGCTAAAAGGAGCGCTCCTCCAAATCCCT
                                                                CCTAGGGAACGTGCTCGACATCGATGACGACTTCCGCCACCCGCAAGCGCAGCGCAC
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Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford (30x, UK
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
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compared to variant clone"
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                                                                                                                                                                                                                                                                                                                                                                                                           /note="results in isoleucine to methionine compared to variant clone"
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/replace="t"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 3;
.2e-113;
es 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="compared to variant clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 608.6; D. Pred. No. 7.2e-0; Mismatches
                   variant type I"
/protein_id="AAM13392.1"
/db_xref="G1:20152845"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="results in serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="nAcRalpha-30D"
                                                                                                                                                                                                                                                                                          gene="nAcRalpha-30D"
                                                                                                                                                                                                                                                                                                                                                                                          gene="nAcRalpha-30D"
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Best Local Similarity 64.3%;
Matches 946; Conservative
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substitution;

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1393 AACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATA 1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1333 ATCGATGTGGACGAGAAAATCAATTGCTAGTCACTAATGTGTGTTAAAACTGGAGTGG 1392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGATGAAACTGGCGGTGATATCAGCAGTTACGTGCTCAACGGCGAGTGGGAACTACTG 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACCCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                571 CAGGATGAAGGGGGGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAATA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGTCCCCGGCAAGGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCGAC 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 CCCGTCGTCAACGAGAGCGACCCGCTGCAGCTCTCCGCCTCACGCTCATGCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 ATCGACGTGGACGAGAAGCCAGCTTTTAATAACAAACATCTGGCTAAAACTAGAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 CCCGGCATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCCTTCGACGACCAA
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                                                                                                                                                                                                                                                                                                                                                                                /note="results in deletion of asparagine and serine;
compared to B allele"
/replace=""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="results in asparagine to serine substitution;
compared to B allele"
/replace="g"
                                                                                                                                                                                                                                                             /note="results in lysine to argenine substitution;
compared to B allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="results in serine, glycine, and asparagine insertion; compared to B allele" /replace="agoggcaac" 1121
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                      /note="results in phenylalanine to isoleucine substitution; compared to B allele"
                                                                                                                                        to isoleucine
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Pred. No. 7.7e-108;
0; Mismatches 422;
                                                                                                               /gene="nAcRalpha-34E"
/note="results in threonine
compared to B allele"
gene="nAcRalpha-34E"
                                                                                                                                                                                                                                    /gene="nAcRalpha-34E"
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                                                                /replace="c"
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                                                                                                                                                                                   AF272778 29-APR-2002 Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5 subunit (nAcRalpha-34E) mRNA, nAcRalpha-34E-A allele, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NMLSPKTAAAATAAGDEATTQQPTNIELCARKRQRLERRKKKRATPRETDIKKQQQL
SMPPFKTRKSTDTYSTPAATTSCPTATYMQCRASDNEFSIPISRHDRVSTATFAWVLH
VLQVLLVSLQQWQLHVQQRSVLLFRRIAASTTAFISYLGSFRAQLKNSSSSSSSNSS
NNSSTQILINGINKHSWIFLITINILESKVCLLAGPHEKRLLHDLLDPYNTLERPVLNES
DNLQLSFGLTLMQILIDYDEKNQLLVTNVWLKLEWNDNNLRWNTSDYSGVKDLRIPPHR
IWKPDVLMYNSADEGFDGTYQTNVVVRNNGSCLYVPPGIFKSTCKIDITWPFPDDQRC
EMKFGSWTYDGFQLDLQLQDETGGDISSYVLNGEWELLGVPGKRNEIYYNCCPEPYID
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MVAETWAPTSCBAVPLLGTYRVCIMFWYASSVYTILLINYHIRNADTHEMSFRIRIYF
MVAETWAPTSCBAVPLLGTYFRVCIMFWYASSVYTILLINYHIRNADTHEMSFRIRIYF
LOUFPWILRMSRPGRPLIEPFTTPCSDTSSERKHQILSDVELKERSSKSLLANVLDI
DDDFRHNCRPMTPGGTLPHNPAFYRTVYGGODDGSTGPIGSTRMPDAVTHTCIKSST
EYELGLILKEIRFITDQLRKDDECNDIANDWRFAAMVVDRLCLIIFTMFAILATIAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="G1:20152840"
/translation="MKNAQLKLTEVDDDELWLAVRLAHCSSNFSSSSTRTTSSNQRH
NQQLTTLQPRSLSTKHHSNIASBQHNSQQQEPASKDEDVANHGRSNDQQTHLQQLDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cases 1 to 2907)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford OXI 3QX, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="ion channel; neurotransmitter transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
                   CGTGCTGTCCGCGCCACACATCATGGTG 1485
                                               1827 GGTGCTGCTCTCCGCACATAATCGTG 1857
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/note="compared to B allele"
/replace="a"
375
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/gene="nAcRalpha-34E"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuoidea; Heliothinae; Heliothis.

1 (bases I to 3029)
Schulte,T., Oellers,N. and Adamczewski,M.
Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLWKPDVLMYNSÄDEGFDGTYQTNVVVRSGGSCLYVPPGIFKSTCKMDIAWFPFDDQH
COMRKGSWYNTOROQLDLVLKDEAGGDLSDFITNBGWYLIGMPGKKNTTTYACCPBTY
DVYFTIMIRRERLY PPENLIYPCVLISSMALLGFTLEPDSGEKLTLGYTILSETTYA
NLVAFTLPQVSDAIPLLGTYFNCIMFWVASSVVLTVVVLNYHHRTADIHBMPQMIKSV
FLOMIPWILMSRPGKKITTKTIMMYMTRRELLEKERSSKSTLANVLDIDDDRPHGPP
PROSTGRUGGSGSTFRTDFRRSFVRPSTMEDVGGGLGSHHRELLLIRELGPTTA
RMKKADBEABLISDWKFPAMVVDFCLLFVFTLFTIIATVAVLLSAPHIIVQ**
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Seplevregltlootidvdeknollitniwlslewndynlrwndseyggvkdlripn
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/product="putative nicotinic acetylcholine receptor alpha
7-2 subunit"
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Pred. No. 4.6e-106;
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                                                                                                                                                                                                                                                  2 (bases 1 to 3029)
Schulte, T., Oellers, N. and Adamczewski, M.
Direct Submission
Submitted (19-APR-1999) ZF-BTB, Bayer AG,
51368, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Heliothis virescens"
|mol_type="mRNA"
|db_xref="taxon:7102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAD32698.1"
/db_xref="GI:4895007"
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/note="hvnachra7.2"
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AF143847.1 GI:4895006
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                                                       ATCACGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCGTG
                                                                                                    Arcaccrrceccarcarcarcecceaegaecacreracrarrrcrrcaaecrearcara
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CACGAGAAGAGACTCCTGAACGCGTTGCTGGCGAACTACAACACCCTGGAGCGACCGGTG 217
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                                       Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
1 (Bases I to 3109)
Martin,A., Nadja,E. and Thomas,S.
Nucleic acid encoding insect actyl choline receptor subunit:
Patent: JP 2000023680-A 3 25-JAN-2000;
                                                                                                                                                                                                                                  Heliothis virescens
JP 2000023680-A/3
25-JAN-2000
26-APR-1999 JP 1999118159
04-MAY-1998 DE 19819829.9
MARTIN ADAMUTSUEUSUKI,NADJA ERASU,THOMAS SCHULTE PC
15/09,AOIK67/033,CO7K14/705,CO7K16/28,CI2N1/21,CI2N5/10,
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Location/Qualifiers
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/organism="Heliothis virescens"
/mol_type="genomic DNA"
/db_xref="taxon:7102"
Heliothis virescens (tobacco budworm)
Heliothis virescens
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Best Local Similarity 64.6
Matches 929, Conservative
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OS Helj

PN JP 2

PD 25-5

PF 26-F

PF 04-N

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Larity 64.6%; Pred. No. 4.6e-106;
Conservative 0; Mismatches 460;
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/note="unnamed protein product"
                                                                                                   virescens"
_DNA"
                                                                                             /organism="Heliothis v
/mol_type="unassigned
/db_xref="taxon:7102"
                                   Location/Qualifiers
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'n. 156 217 216 277 276 337 336 397 396 457 456 517 516 577 576 637 989 697 969 757 756 817 816

> 06-SEP-2000 Adamczewski, M.D., Schulte, T.D. and Oellers, N.D. Nucleic acids encoding acetylcholin-receptor subunits from insects Patent: EP 0962528-A 5 08-DEC-1999; Heliothis virescens Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Noctuoidea, Noctuidae, Heliothinae, Heliothis. PAT linear DNA Heliothis virescens (tobacco budworm) Sequence 5 from Patent EP0962528. AX009614 AX009614.1 GI:9996846 DEFINITION ORGANISM AUTHORS TITLE JOURNAL ACCESSION VERSION AX009614 LOCUS KEYWORDS REFERENCE

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GATATGAAGTTCGGTAGGTGGACATATGACGGCAATCAGTTGGATCTGGTGCTAAAAGAT GAAGGGGGCGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGAGTTAATAGGAGTC

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.1654

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codon_start=

Dalpha7"

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'n,

Gaps

Indels 111; Length 1683;

Score 568.4; DB 3; Pred. No. 9.9e-105; 0; Mismatches 416;

38.2%; 65.0%;

Conservative

91 131 151

190 210 250 270

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271 311

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AACGATATGAATCTTCGATGGAATTCGAGTGGTTCGGTGTGTGCGGGATCTGCGAATT

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Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WCIE 6BT, UNITED
                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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1. .1683
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Millar, N.S

REFERENCE AUTHORS

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FEATURES

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Accession Number AE003626" /replace="C" 1605 /obse="nAcRalpha-30D" /note="compared to the sequence deposited in GenBank Accession Number AE003626" /replace="c" /replace="c" /replace="c" /replace="c" /replace="compared to the sequence deposited in GenBank /note="compared to the sequence deposited in GenBank Accession Number AE003626"	Match local S es 946	387 ¢C¢¢¢TG¢¢G¢G¢G¢G¢TGT¢G¢TGT¢T¢TGT¢GTT¢T¢G¢GGATAATTAAGA 446 81 GG¢A¢G¢TG¢GGGTA¢CAGGGCTA¢CTG¢A¢CACCTATTGGA¢CACTACAAGGT 140 81 GG¢A¢G¢TG¢GGGGAGAGAGGGGCTA¢TGCACCACTACAAGGT 140 447 AAGCTGT¢AAGAGCG¢CTG¢TGCTGATG¢T¢CACCTACAATA¢ 506	141 ACTGGAGAGGCCCGTCGTCAACGAGAGCCACCCGTGCAACTCTCGGCCTCACGCT 200	GCAGCAGATCATCGACGTGGATGAAAGAATCAGATTCTGACCACAAATGCGTGGTTAAATGGACGAGAAGAAACCAGCTTTTAATAACAAACATCTGGCTTAAAACTAGAGTGGAATGATGGACGAGAAGAACCAGCTTTTAATAACAAACATCTGGCTTAAAACTAAAGGAATGA TTTGGACGAGAAGAAATCAGCTTCTCATAGAGTTCGATGGAACGA	TATGAACTTGAGGTGGAACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAGTGCCACC 33	396 CANGUTATICAACGAACGTGGTGGGGAACAACGGCTCGTGTCTGTACGTGCGCCCCCGG 455 807 CACGTATCAACGACTTGTGGTCAAACGTAGCGCAGTTGTTGTTGTGTGCCCCCCCGG 866 456 CATCTTCAAGAGCACCTGCAACATCGACATCACCTGGTTCCCCTTGGACGACCAACGAG 866 456 CATCTTCAAGAGCACCTGCAAGATCGACATCACCTGGTTCCCTTTGAACGACGACAACGT 515 867 TATCTTCAAGAGCACTGCAAGATGGAATTGATCACTTGATGATGACCAACATTG 926 516 CGAGATGAAGTTTGGCAACATGGAACTTATGATGGATCTACAACTACAACTACAAGA 575	927 CGAAATGAAATTCGGTAGTTGGACTTACGATGGAAATCAGTTGGATTTGGATTTGAATTC 986 576 TGAAGGGGGGGGAGATATAAGCAGTTTTGTCACGAATGGCGAATGGGGAGTTAATAGGAGT 635 677 CGAAGATGGAGGGAGTTTTCTCACGATTGTAGGAGTTAATAGGAGT 635 687 CGAAGATGGAGGGGATCTTTCCGATTTCATAACAAATGGCGAGTGGTACTTGCTTG	636 CCCCGGCAAGCGCAACGAGATCTACTACTAGTTGTCCGGAGCCATACATCGACATCAC 695	756 CGTGCTCATCGCCTCCATGGCTCTATTGGGGTTCACCTTGCCTCCAGACTCCGGAGAAA 815
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Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putarive Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphas, Dalphas and Dalpha7, in Drosophila melanogaster Identify
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-1 Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)
11973307
                                                                                                                                             GACGATGCCAGCGACGTCGCAGCGCCTTTGCTCGGCACCTACTTCAACTGCATCAT
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816 GTTGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGGTGGCGGA
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Drosophila melanogaster
Eukaryota; Mutazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Moeptera; Endopteryryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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GenCore version 5.1.6
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US-09-303-232-3_COPY_335_1822 1488 Title: Perfect score:

1 atgggcgggcgggcgccg.........cgccacacatcatggtgtcg 1488 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6747726 Total number of hits satisfying chosen parameters:

3373863 segs, 2124099041 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries Database

N Geneseq 29Jan04:*

1: geneseqn1980s:*
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SUMMARIES

Aat48235 Neuronal	Abk92165 Prostate	Ada10854 Human neu	Adc71170 Human 205	Adc71168 Human 205	Abl07799 Drosophil	Aat48236 Neuronal	Adal0856 Human neu	Aac90382 Chimeric	Adb78675 Human nic	Adb78664 Human nic	Adb78674 Human nic	Adb78676 Human nic	Aad26345 Human mut	Adb78665 Human nic	Adb78666 Human nic	Adb78678 Human nic	Aas91552 DNA encod	Aat59527 Alpha4 su	Abs54871 Human neu	Abv73244 Human neu	Aav12200 Human neu
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20.8	20.8	20.8	20.8	20.8	20.3	19.6	19.6	19.5	19.5	19.5	19.4	19.4	19.3	19.3	19.3	19.3	19.2	19.2	19.2	19.2	19.2
309.2	309.2	309.2	309.2	309.2	302.4	292	292	g	289.8	89	288.2	288.2	286.6	286.6	286.6	286.6	286.2	286.2	285.2	285.2	285.2
24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Acetyl-choline receptor; nicotinic; insect; insecticide; screening; neurotransmission; plant protection agent; conductance; AChR; ds.
                                                         H. virescens acetyl-choline receptor DNA from clone Hva7-1.
                                                                                                                         /*tag= a
/product= "acetyl-choline receptor"
              BP
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              AAZ24476 standard; cDNA to mRNA; 3700
                                                                                                           Location/Qualifiers
335. .1825
                                                                                                                                                                           98DE-01019829.
                                                                                                                                                                                         98DE-01019829
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                                                                                             Heliothis virescens.
                                                                                                                                                                                                       (FARB ) BAYER AG.
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                                          17-FEB-2000
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                            AAZ24476;
                                                                                                           Key
RESULT 1
       AAZ24476
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Adamczewski M, Oellers N,

WPI; 2000-014207/02. P-PSDB; AAY50815.

New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides.

Claim la; Page 14-17; 26pp; German.

This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as

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insecticides, or (b) genes which encode polypeptides that are involved i formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline receptor isolated from Heliothus virescens
                                                                                                                                       ATGGCGGGCGCGCCGCTCGCACTTGGCGGCGCCCGCGGGGCCTGCTGCTGCTGCTG
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                            This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (I) from insects which can be used as an insecticide. Inhibitors of (I) interfere with neurotransmission. (I) (also vectors containing it, its regulatory regions, and antibodies directed against (I)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (I) are also used to isolate and characterize the specified regulatory regions and for recombinant production of (II). This sequence encodes an acetyl-choline
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                                                                                                                                                                                                                                                                                                                                            This invention describes a novel nucleic acid (NA) encoding a nicotinic acetyl-choline receptor (1) from insects which can be used as an insecticide. Inhibitors of (1) interfere with neurotransassion. (1) (also vectors containing it, its regulatory regions, and antibodies directed against (1)-encoded proteins) are used to screen for: (a) plant protection agents that alter conductance of AChR, potentially useful as insecticides, or (b) genes which encode polypeptides that are involved in formation of functionally related AChR in insects. (1) are also used to recombinant production of (11). This sequence encodes an acetyl-choline receptor isolated from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1476 AACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATA 1535
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Adamczewski M,
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                  766 CCGTGCGTACTGATCGCCTCCATGGCACTGCTAGGGTTTACACTGCCACCAGATTCTGGT
                                                                                                                                                     GAAAAGTTGTCTTTAGGTGTGACGATATTACTGTCGTTGACGGTGTTCCTCAACATGGTG
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  ATCACGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elunidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
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0; Mismatches 225; Indels
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al Similarity 72.9%; Pred. No. 1
605; Conservative 0; Mismatch
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11-JUL-2000; 2000US-00614150
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P-PSDB; ABB69630.
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Best Local Similarity
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4; S 80 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher elekaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7377-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly CICGCACTIGGCGGCCCCGCGGGCCTGCTGCTGCTGTGCCTGCTCTGCCTGCTCTGGCCGAGGG Sequence 1540 BP; 412 A; 390 C; 376 G; 362 T; 0 U; 0 Other; Claim 1; SEQ ID NO 16175; 21pp + Sequence Listing; English from WIPO at ftp.wipo.int/pub/published_pct_sequences 30.8%; Score 458.2; DB 4; 60.1%; Pred. No. 9.6e-102; iive 0; Mismatches 493;

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                                               GTCACGGCCCGGCTCGGCGACGCCGCCGCCGCGCGCGTA---CCTCCGCCGCGGA
                                                                                      GGGTCGACCCGGTCGCAAGATTACACGCAAAACAATACTATTAAGCAATCGCATGAAGGA
                                                                                                                                     CCTGGAGCTGCGCGCGCTCCTCCAAGTCGCTCCTAGCGAACGTGCTCGACATGA
                                                                                                                                                                                                                                                                  CGACTTCCGGCACAATATCTGGCTCCCAAACCGCCATTGGCTCGTCGGCCAGCTTCGG
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hydroxytryptamine, 5-HT3; calcium ion conductance; ss.
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                                                                                       CGCCG------CCGGACCTGGAGCTGCGCGAGCGCTCCTCCAAGTCGCTCCTAGCGA
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  Length 1509;
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     Score 405.6; DB 4;
Pred. No. 6.7e-89;
0; Mismatches 604;
  Query Match 27.3%;
Best Local Similarity 56.5%;
Matches 840; Conservative
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mammalian cells or amphibian oocytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs
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                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human neuronal nicotinic acetylcholine receptor nAChR. nAChR's form ligand-gated ion channels that mediate synaptic transmissions between nerve and muscle and between neurons upon interaction with the neurotransmitter acetylcholine. The nucleic acid molecule is useful for identifying compounds that modulate human neuronal nAChR. The present sequence receptor, nAChR, alpha 7 subunit. Note: the present sequence decodes to the protein shown in ADA10874 not the one described in the specification
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                                                                                                                                                  New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human neuronal nicotinic acetylcholine receptor (nAChR), useful for ident: compounds that modulate human neuronal nAChR activity.
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Pred. No. 7.3e-89;
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                                                              nicotinic acetylcholine receptor
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Pred. No. 9.1e-89;
1; Mismatches 604;
                                                                                                                                                                                                                                                                                          (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                            "neuronal
location/Qualifiers
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alpha-7 subunit"
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 TGGCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCCTCCTGCAGATCATGG 262
                                                                                                                                                    CCCACAGACTATGGAAACCAGACGTCCTTATGTACAACAGCGCGGACGAAGGGTTCGACA 394
                                                         A------GGCAGATATCAGTGGCTATATCCCCAATGGAGAATGGGACCTAGTGGGAA
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                              ACGTGGACGAGAAGAACCAGCTTTTAATAACAAACATCTGGCTAAAAACTAGAGTGGAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
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                                                                                                                                     7 subunit cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying antagonists or agonists of human neuronal nicotinic acetylcholine receptors, by contacting recombinant cells with test compound, and measuring ion flux of cells or binding of compound to NNACHR.
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                                                                                                                                                                acetylcholine receptor; nNAChR;
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                                                                                                                                    receptor alpha
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Pred. No. 9.1e-89;
L; Mismatches 604;
                                                                                                                                  Human neuronal nicotinic acetylcholine
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30-NOV-1992;
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neuronal nicotinic acetylcholine receptors, useful for in vitro screening
of a drug substance in a test system specific for humans.
ATTCTGAAGGAGATTA
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The present invention describes an isolated antibody that binds to one of the human PRO proteins designated PR0212, PR029, PR0341, PR0535, PR0619, PR01030, PR08099, PR0830, PR06183, PR06109, PR01087, PR01091, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR02185, PR01081, PR01081, PR01081, PR02185, PR02185, PR01081, PR01081, PR01081, PR02185, PR02185, PR01081, PR01081, PR02185, PR02185, PR01081, PR01081, PR02185, PR02185, PR01081, PR01081, PR01081, PR01081, PR02185, PR02185, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, PR01081, P
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alpha7 ligand gated ion channel coding sequence

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2000WO-US011862.

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Human, alpha7 nicotinic acetylcholine gated ion channel; 5-hydroxytryptamine; 5-HT3; calcium ion conductance; 88.
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                                                                                                                        Berkenpas
                                                                                                                                                                                                                                                                                                                                                                                       Claim 50; Page 69; 77pp; English.
                                                          (PHAA ) PHARMACIA & UPJOHN CO
99US-0136174P.
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                                                                                                                  Groppi VE, Wolfe ML,
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   27-MAY-1999;
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RESULT 13 AAC90385 ID AAC90385 standard; cDNA; 1509

mutant;

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Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the coding sequence for a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptemine (5-H73) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-H73 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells. The protein encoded by this sequence has the wild-type cysteine residue at position 241 substituted by a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCCCGCGGGGCCTGCTGCTGCTGTGCCTGTCTGGCCGAGGGGGGCACGCTGCGGGT
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                                                                                                                                                                                                                                                                                                                              Human; alpha? nicotinic acetylcholine gated ion channel;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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Pred. No. 1.7e-88;
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Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.
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                                                                                                                   AGTICGCCGCCTGTGTGGTGGACCGCCTGTGCCTCATGGCCTTCTCGGTCTTCACATCA
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5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
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	Search completed: May 7, 2004, 15:01:41	comple	Search
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1441	1382 AGTICGCCGCCTGTGTGTGGTGGACGCCTTGTGCCTCATGGCCTTTTCTCGCTTTTCACCATCA 1441	138	qq
1441	2 AGTICGCCGCCAIGGICGIGGACAGACIGIGGCCITATIAICITIACCTGIICACAAICA	138;	ζζ
1381	1322 GCTACATTGCCAATGCTTCCGCTGCCAGGACGAAAGCGAGGCGGTCTGCAGCGAGTGGA 1381	132	qq
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1321	1262 TGCACGGCGGGCAACCCCCGAGGGGGACCCGGACTTGGCCAAGATCCTGGAGGAGGTCC 1321	126.	Ωp
1321	1286 TCGACTACGAGCTCTCCCTCATTCTGAAGGAGATTA 1321	128	δ
1261	1202 CCGACTCTGGGGTAGTGTGTGGCCGCATGGCCTGCTCCCCCACGCACG	120	qq

Search completed: May 7, 2004, 15:01:4 Job time : 609.456 secs

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RESULT 1							
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VERSION	BG6.	32919.1	GI:13	7584	60		
SOURCE		sophila	melano	gast	fruit	fly)	
ORGANISM		sophila aryota;	melanc Metazo	gast a, A	ster Arthropoda; He	exapoda;	Insecta; Pterygota;
	Eph	ydroide	Dros	ophi	lidae; Drose	brachyce bhila.	uscomorpina;
AUTHORS	Har	(bases vey, D.,	L to 88 Brokst	ein,	Hong, L	., Evans-Holm,M.,	Su,C., Tsang,G.,
TITLE	BDG	BDGP/HHMI Drosophila	rosoph	n, G.R tila E	ST Project	ш	
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been removed. hit
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                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH5 - alpha"
/clone lib="dH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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                                                                                                                                                                                                                                                                                                      Score 476.2; DB 12; Length 885;
Pred. No. 8.9e-82;
); Mismatches 223; Indels 0;
more T residues at the beginning of the sequence, polyadenylated. The resulting Poly-T sequence has genomic AE003511: arm:X [18792641,19136447] estimated-cyto:1884] lescimated-cyto:1884] lescimated-cyto:1841 row: C column: 2 High quality sequence stop: 784.
                                                                                                                  'organism="Drosophila melanogaster"
                                                                                                                                                                           'sex="male and female"
                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="GH16126"
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Contact: Genoscope Genoscope Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r For more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODD007CH03QPI&cluster=7646.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODD007CH03QPI.
                                                                                                                                                                                                                                                                                                                                                                            AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CSODD007YP05 5-PRIME, mRNA sequence.
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GGCACCTACTTCAACTGCATCATGTTCATGGTGGCTTCCTCCGTCGTCTCCCACCATACTG 972
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/clone_lib="Homo sapiens NEUROBLASTOMA_COT_50-NORMALIZED"
/note="list strand oDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
                                                              165 GGAACTTATTTCAATTGCATTATGTTTATGGTGGCCTCATCAGTTGTGTCAACCATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGCTCCGGGACTCAACATGCGCTGCTCGCCGGAGGTNCTGGCTGGCGCTGGCCGCT
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Pred. No. 1.4e-51;
5; Mismatches 360; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Lill-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DD007YP05"
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589 399 519

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/organism="Homo sapiens"
//mol types="mRNA"
//db xref="taxon.9606"
/clone_lib="Single gene library"
//note="vector: pDrive Cloning Vector, RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pDrive Cloning vector and sequenced completely vaing MI3 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."
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PCR isolation and cloning of novel spli
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Location/Qualifiers
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Contact: Jin, P.
Incyte Corporation
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Tel: 650 621 8639
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LIYVELLVITETIPSTSLVIPLIGEYLLFTMIFVTLSIVITVFYLDSDCGEKVTLCISVLLS
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AQNVAKEIQDDMKYVAMVIDRIFLWVFILVCILGTAGIFLQPLMARDDT"
                                                                                                                                               Submitted (IG-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="eyeball"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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Toya,T., Yasunishi,A.,
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0; Mismatches 469; Indels
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/clone="E130103E14"
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/organism="Mus musculus"
                Sogabe, Y., Tagami, M., Tagawa, A.,
Takeda, Y., Tanaka, T., Tomaru, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
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AK053497
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (Dases I to 1864)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Ronno, H., Akiyama, J., Nishi, K., Tsahiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamra, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yanjuake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watsahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Strikn integrated sequence analysis (RISA) system-384-format genome Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2916)
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                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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Please visit our web site for further details.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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/db_xref="MGI:24\overline{2}0066"
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URL:http://fantom.gsc.riken.go.jp/
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Direct Submission
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2916 bp mRNA linear HTC 20-SEP-2003
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
enriched library, clone:10300648406 product:NEURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                  GGAATGATATGAACTTGAGGTGGAACACTTCAGATTTCGGCGGGGTCAAAGATTTAAGAG
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3126 bp mRNA linear HTC 19-SEP-2003
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A73007P14 product:NBURONAL NICOTINIC
ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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TTAAAGCCCCGGGGCTACAAACATGAAATCAAGTACAACTGCTGTGAGGAGATCTACCAAG
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                                                           ACATCACGTTTGCGGTGGTGATCCGGAGGAAAACGCTCTACTACTTCTTCAATCTGATCG
                                                                                                                 <u> acarcaceracectaracatroeceecreeceererreracacearcarcarcarca</u>
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RPVANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLMLKQIMNDYKLKMKPSDYGGVEF
MRVFAEKIMKPDIVLYNNADGDFQVDDKTKALLKYTGEVTWIPPAIFKSSCKIDVTYF
                                                                                                                                                                                                                                                                                                                                                                                                                                               PFDYQNCTMKFGSWSYDKAKIDLYLIGSSMNLKDYWESGEWAIIKAPGYKHEIKYNCC
EEIYQDITYSLYIRRLPLFYTINLIIPCLLISFLTVUVFYLPSDCGEKVTLCISVLLS
LTVFLLVITETIPSTSELVIPLIGEYLLFTMIFWTLSIVITYSTUNHYRTPTTHRFT
WKAVFLINLLPRWMFWTFYSTEEDBYTRNFYGALISNLNCFSRADSKSCKEGYPCO
DGTCGYCHHRRVKISPRSANLTRSSSSESVDAVLSLGALSPEIKEALOSVKYIAENMK
AQNVAKEIQDDWKYVAMVIDRIFLWVFILVCILGTAGLFQPLMARDDT"
                                                           enriched mouse cDNA library'
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Pred. No. 6.8e-44;
); Mismatches 469; Indels
                      tissue type="spinal ganglion"

clone lib="RIKEN full-length of a stage="12 days embryo"
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